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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:04:52 ; Search time 57 Seconds

(without alignments)
679.105 Million cell updates/sec

Title: US-10-023-282-310

Perfect score: 137

Sequence: 1 MRTGGLPVLVLLLAGAPAA.....CNALEYPIPTVTVLPDRQX 137

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq 29Jan04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	99.3	136	3 AAB18925	Aab18925 A novel p
2	136	99.3	136	3 AAB28612	Aab28612 Human C17
3	136	99.3	136	5 ABB84572	Abb84572 Human PRO
4	136	99.3	136	5 ABB95578	Abb95578 Human ang
5	136	99.3	136	6 ABB95578	Abb95578 Human ang
6	136	99.3	136	6 ABB95578	Abb95578 Human ang
7	136	99.3	136	6 ABO19435	Abol19435 Human sec
8	136	99.3	136	6 ABO19435	Abol19435 Human sec
9	136	99.3	136	6 ABR39861	Ab39861 Human HEM
10	136	99.3	136	6 ABR39861	Ab39861 Human HEM
11	136	99.3	136	6 ABR39861	Ab39861 Human HEM
12	136	99.3	136	6 ADA76590	Ada76590 Novel hum
13	136	99.3	136	6 ADA76590	Ada76590 Novel hum
14	136	99.3	136	6 ABO25143	Abol25143 Human sec
15	136	99.3	136	7 AAB39113	Aab39113 Human PRO
16	136	99.3	136	7 AAB39113	Aab39113 Human PRO
17	136	99.3	136	7 ADC29821	Adc29821 Novel hum
18	136	99.3	136	7 ADD10601	Add10601 Human sec
19	136	99.3	136	7 ADD10601	Add10601 Human sec
20	136	99.3	136	7 ABO37354	Abol37354 Human sec
21	136	99.3	136	8 ADA41562	Ada41562 Human sec
22	136	99.3	137	2 AAW88595	Aaw88595 Secreted
23	136	99.3	137	4 ABO50362	Abol50362 Human sec
24	136	99.3	137	6 ABO44619	Abol44619 Novel hum
25	136	99.3	137	7 ABO26099	Abol26099 Human pro

26	63	46.0	112	4	ABB51287	Abb51287 Human sec
27	18	13.1	136	6	ABP70606	Abp70606 Amino aci
28	18	13.1	136	6	AAO16399	Aao16399 Bovine C1
29	18	13.1	136	6	ABU08233	Abu08233 Mouse Pro
30	18	13.1	139	6	AAO16400	Aao16400 Murine C1
31	18	13.1	139	6	ABR39862	Ab39862 Murine HE
32	8	5.8	23	2	AAK31606	Aak31606 Protein X
33	8	5.8	30	2	AAK31606	Aak31606 Protein X
34	8	5.8	90	2	AAK31606	Aak31606 Protein X
35	8	5.8	105	2	AAK31606	Aak31606 Protein X
36	8	5.8	105	2	AAK31606	Aak31606 Protein X
37	8	5.8	105	2	AAK31606	Aak31606 Protein X
38	8	5.8	122	5	ABY36660	Ab36660 Fragment
39	8	5.8	131	2	AAK31606	Aak31606 Protein X
40	8	5.8	131	2	AAK31606	Aak31606 Protein X
41	8	5.8	140	4	ABG01615	Abg01615 Novel hum
42	8	5.8	197	5	AAO20967	Aao20967 Human 197
43	8	5.8	208	2	AAK31236	Aak31236 Human Apo
44	8	5.8	240	5	ABP70130	Abp70130 Human NOV
45	8	5.8	261	5	ABG91404	Abg91404 Primate L

ALIGNMENTS

RESULT 1

AAB18925

ID AAB18925 standard; protein; 136 AA.

AC AAB18925;

XX 08-FEB-2001 (first entry)

XX A novel polypeptide designated PRO4425.

DE A novel polypeptide designated PRO4425.

XX Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;

KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4356; PRO4355;

KW PRO4352; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;

KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;

KW insulinemia; kidney disorder; Betgers disease; nephropathy;

KW Schonelein-Henoch purpura; celiac disease; dermatitis herpetiformis;

KW Crohns disease.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

FT Peptide

FT 1..19

FT /note= "signal sequence"

FT Modified-site

FT 16..22

FT /note= "N-myristoylation site"

FT Modified-site

FT 60..69

FT /note= "tyrosine kinase phosphorylation site"

XX WO200056889-A2.

XX 28-SEP-2000.

XX 01-MAR-2000; 2000WO-US005601.

XX 23-MAR-1999; 99US-012577AP.

XX 23-MAR-1999; 99US-012577AP.

XX 24-MAR-1999; 99US-012582AP.

XX 31-MAR-1999; 99US-0127035P.

XX 05-APR-1999; 99US-0127706P.

XX 21-APR-1999; 99US-0130359P.

XX 27-APR-1999; 99US-0131270P.

XX 27-APR-1999; 99US-0131272P.

XX 27-APR-1999; 99US-0131291P.

XX 04-MAY-1999; 99US-0132371P.

XX 04-MAY-1999; 99US-0132379P.

XX 04-MAY-1999; 99US-0132383P.

XX 25-MAY-1999; 99US-0135750P.

XX 08-JUN-1999; 99US-0138166P.

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Wed Feb 25 11:56:33 2004

PR 20-JUL-1999; 99US-0144791P.
 PR 03-AUG-1999; 99US-0146970P.
 PR 09-DEC-1999; 99US-0170262P.
 XX (GETH) GENENTECH INC.
 XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2000-628263/60.
 DR N-PSDB; AAA96352.
 XX Novel secreted and transmembrane polypeptides useful for diagnosing tumor
 PT in a mammal, for identifying agonists and antagonists of the polypeptide
 PT and for therapeutic use.
 XX Claim 12; Fig 34; 222pp; English.
 XX The present sequence represents a secreted or transmembrane polypeptide.
 CC The specification describes polypeptides designated PRO1484, PRO4334,
 CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
 CC PRO4356, PRO4352, PRO4380, PRO4384, PRO4408, PRO4425, PRO5990,
 CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
 CC useful for diagnosing tumor in a mammal. The polypeptides, their
 CC agonists and antagonists are useful treating a condition associated with
 CC expression or activity of the polypeptide. Conditions treated include
 CC obesity, diabetes or hypo-insulinemia. The polypeptides are
 CC capable of inducing proliferation of mammalian kidney mesangial cells and
 CC are therefore useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Bercers disease or other
 CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
 CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
 CC to generate transgenic animals for use in development and screening of
 CC therapeutically useful reagents and also for chromosome identification
 CC and tissue typing
 XX Sequence 136 AA;
 SQ
 Query Match 99.3%; Score 136; DB 3; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPTGGLPVLLLLLAGAPAAAPPTPTCYSRMRALSOEITRDNFLLOVSEPCVRYLPR 60
 DB 1 MPTGGLPVLLLLLAGAPAAAPPTPTCYSRMRALSOEITRDNFLLOVSEPCVRYLPR 60
 QY 61 LYLDIHNYCVLDKLRDFVASPPCKWQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 DB 61 LYLDIHNYCVLDKLRDFVASPPCKWQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPVTVLPDRQR 136
 DB 121 LEYPIPVTVLPDRQR 136
 RESULT 2
 ID AAB28612 standard; protein; 136 AA.
 XX AAB28612;
 AC AAB28612;
 DT 12-FEB-2001 (first entry)
 XX Human C17 polypeptide.
 XX Human; C17; haemopoietic stem/precursor cell; HSPC;
 KW mesenchymal stem cell division; DNA fingerprinting; bone disease.
 XX Homo sapiens.
 OS
 XX WO200063382-A1.
 PN
 XX 26-OCT-2000.
 PD

XX 14-APR-2000; 2000WO-US009904.
 XX 15-APR-1999; 99US-0129463P.
 PR (OSIR-) OSIRIS THERAPEUTICS INC.
 XX Liu X, Cheng L;
 XX WPI; 2000-647518/62.
 DR N-PSDB; AAC65370, AAC65371.
 XX New isolated nucleic acid encoding a human hematopoietic stem/precursor
 PT cell polypeptide called C17, for increasing the rate of multiplication of
 PT mesenchymal stem cells in vitro and for chromosome mapping and DNA
 PT fingerprinting.
 XX Claim 16; Fig 2; 68pp; English.
 XX The present sequence is a human haematopoietic stem/precursor cell
 CC (HSPC) polypeptide called C17. The C17 polynucleotide may be used to
 CC increase the rate of multiplication of human mesenchymal stem cells in
 CC vitro and to determine the presence of growth-stimulating receptors on
 CC the surface of a cell. The C17 polypeptide may be used to generate
 CC polyclonal sera or monoclonal antibodies specific for C17. The
 CC polynucleotide is used as a marker for chromosome mapping and DNA
 CC fingerprinting. It is also used in detecting genetic mutations in order
 CC to diagnose diseases, such as those affecting bone formation
 XX Sequence 136 AA;
 SQ
 Query Match 99.3%; Score 136; DB 3; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPTGGLPVLLLLLAGAPAAAPPTPTCYSRMRALSOEITRDNFLLOVSEPCVRYLPR 60
 DB 1 MPTGGLPVLLLLLAGAPAAAPPTPTCYSRMRALSOEITRDNFLLOVSEPCVRYLPR 60
 QY 61 LYLDIHNYCVLDKLRDFVASPPCKWQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 DB 61 LYLDIHNYCVLDKLRDFVASPPCKWQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPVTVLPDRQR 136
 DB 121 LEYPIPVTVLPDRQR 136
 RESULT 3
 ABB84972
 ID ABB84972 standard; protein; 136 AA.
 XX ABB84972;
 AC ABB84972;
 DT 16-MAY-2002 (first entry)
 XX Human PRO4425 protein sequence SEQ ID NO:312.
 XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombopilebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX Homo sapiens.
 OS
 XX WO200200690-A2.
 PN
 XX 03-JAN-2002.
 PD

PF 20-JUN-2001; 2001WO-US019692.
 XX 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00808689.
 PR 05-APR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PA (GETH) GENEVENTECH INC.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR N-PSDB; ABL88227.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 11; Fig 312; 565pp; English.
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABL84817 to
 CC ABL85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis [such as breast carcinoma and liver carcinoma] and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX Sequence 136 AA;
 SQ
 Query Match 99.3%; Score 136; DB 5; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTGGLPVLLLLAGAPAAAREPTPTTCYSRMALSQEITRDNFLLQVSPSPCVRYLPR 60
 DB |||||
 QY 1 MRTGGLPVLLLLAGAPAAAREPTPTTCYSRMALSQEITRDNFLLQVSPSPCVRYLPR 60
 DB |||||
 QY 61 LYLDIHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
 DB |||||
 QY 61 LYLDIHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
 DB |||||
 QY 121 LEYPIPVTTVLPRQR 136
 DB |||||
 QY 121 LEYPIPVTTVLPRQR 136
 DB |||||
 RESULT 4
 ABB95578
 ID ABB95578 standard; protein; 136 AA.
 XX
 AC ABB95578;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related protein PRO4425 SEQ ID NO: 312.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US021735.
 XX
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00808689.
 PR 05-APR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX

PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-171999/22.
 DR N-PSDB; ABL95716.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 312; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention
 XX
 SQ Sequence 136 AA;
 Query Match 99.3%; Score 136; DB 5; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRTPGPLPVLLLLLAGAPAAARPTPTTCYSRMALSOEITRDFNLLQVSESEPCVRYLPR 60
 Db 1 MRTPGPLPVLLLLLAGAPAAARPTPTTCYSRMALSOEITRDFNLLQVSESEPCVRYLPR 60
 QY 61 LYLDIHNVCVLDKLRDFVASPPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 Db 61 LYLDIHNVCVLDKLRDFVASPPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPVTTVLPRQR 136
 Db 121 LEYPIPVTTVLPRQR 136
 RESULT 5
 ABP70605
 ID ABP70605 standard; protein; 136 AA.
 XX
 AC ABP70605;
 XX
 XX 22-APR-2003 (first entry)
 XX
 DE Amino acid sequence of human secreted polypeptide designated PRO4425.
 XX
 KW Human; secreted polypeptide; PRO4425; bone disorder; osteoarthritis;
 KW bone damage; cartilage damage; osteoporosis; osteomyelitis;
 KW osteogenesis imperfecta; rheumatoid arthritis.
 XX
 OS Homo sapiens.11.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Modified-site 16..22
 FT /note= "N-myristoylation site"
 FT Modified-site 60..69
 FT /note= "tyrosine kinase phosphorylation site"
 XX
 PN WO2003000729-A2.
 XX
 PD 03-JAN-2003.
 XX
 EF 13-DEC-2001; 2001WO-US048938.
 XX
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Wood WI, Ye W, Zhang Z;
 XX
 DR WPI; 2003-175282/17.
 DR N-PSDB; ABZ68432.
 XX
 PT New secreted nucleic acid encoding a polypeptide, designated PRO4425, for
 PT treating bone disorders, such as, osteoarthritis, damage through trauma,
 PT osteoporosis, osteomyelitis, osteogenesis imperfecta, or rheumatoid
 PT arthritis.
 XX
 PS Claim 10; Fig 2; 93pp; English.
 XX
 CC The present sequence represents a human secreted polypeptide, designated
 CC PRO4425. The polypeptide has a calculated molecular weight of 15577
 CC daltons, and a structure that is similar to the interleukin-8 family of
 CC proteins. The PRO4425 polynucleotide and polypeptide are useful for
 CC treating bone disorders, such as osteoarthritis, damage to the bone or
 CC cartilage through trauma, osteoporosis, osteomyelitis, osteogenesis
 CC imperfecta, or rheumatoid arthritis. The nucleic acids are useful as
 CC hybridization probes, in chromosome and gene mapping, and in generating
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. Both PRO4425 polynucleotide and
 CC polypeptide are useful in tissue typing
 XX
 SQ Sequence 136 AA;
 Query Match 99.3%; Score 136; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRTPGPLPVLLLLLAGAPAAARPTPTTCYSRMALSOEITRDFNLLQVSESEPCVRYLPR 60
 Db 1 MRTPGPLPVLLLLLAGAPAAARPTPTTCYSRMALSOEITRDFNLLQVSESEPCVRYLPR 60
 QY 61 LYLDIHNVCVLDKLRDFVASPPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 Db 61 LYLDIHNVCVLDKLRDFVASPPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPVTTVLPRQR 136
 Db 121 LEYPIPVTTVLPRQR 136
 RESULT 6
 ABU69119
 ID ABU69119 standard; protein; 136 AA.
 XX
 AC ABU69119;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human PRO polypeptide #17.
 XX

KW Human; secreted and transmembrane protein; bone disorder; obesity;
 KW cartilage disorder; sports injury; arthritis; diabetes mellitus;
 KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassaemia;
 KW haemoglobin-associated disorder; kidney disorder; Berger disease;
 KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;
 KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;
 KW antiarthritis; antidiabetic; antianaemic; nephrotropic; antiinflammatory.
 XX Homo sapiens.
 XX US2003032061-A1.
 XX 13-FEB-2003.
 XX 26-DEC-2001; 2001US-00036214.
 XX 15-MAY-1998; 98US-0085579P.
 XX 15-DEC-1998; 98US-0112514P.
 XX 22-DEC-1998; 98US-0113300P.
 XX 23-DEC-1998; 98US-0113430P.
 XX 23-DEC-1998; 98US-0113605P.
 XX 23-DEC-1998; 98US-0113821P.
 XX 23-DEC-1998; 98US-0114440P.
 XX 12-JAN-1999; 99US-0115552P.
 XX 22-JAN-1999; 99US-0116843P.
 XX 23-MAR-1999; 99US-0125774P.
 XX 24-MAR-1999; 99US-0125778P.
 XX 24-MAR-1999; 99US-0125826P.
 XX 31-MAR-1999; 99US-0127035P.
 XX 05-APR-1999; 99US-0127706P.
 XX 13-APR-1999; 99US-0129122P.
 XX 21-APR-1999; 99US-0130359P.
 XX 27-APR-1999; 99US-0131270P.
 XX 27-APR-1999; 99US-0131272P.
 XX 27-APR-1999; 99US-0131291P.
 XX 04-MAY-1999; 99US-0132371P.
 XX 04-MAY-1999; 99US-0132379P.
 XX 04-MAY-1999; 99US-0132383P.
 XX 14-MAY-1999; 99US-0132383P.
 XX 25-MAY-1999; 99US-0135750P.
 XX 08-JUN-1999; 99US-0138166P.
 XX 20-JUL-1999; 99US-0144791P.
 XX 03-AUG-1999; 99US-0146370P.
 XX 29-OCT-1999; 99US-0162506P.
 XX 02-DEC-1999; 99US-0162506P.
 XX 22-DEC-1999; 99US-0162506P.
 XX 01-MAR-2000; 2000US-0030720.
 XX 02-MAR-2000; 2000US-0030720.
 XX 22-MAY-2000; 2000US-0035841.
 XX 02-JUN-2000; 2000US-0035841.
 XX 23-AUG-2000; 2000US-0035841.
 XX 24-AUG-2000; 2000US-0035841.
 XX 01-DEC-2000; 2000US-0035841.
 XX 28-FEB-2001; 2001US-0035841.
 XX 01-JUN-2001; 2001US-0035841.
 XX 20-JUN-2001; 2001US-0035841.
 XX 09-JUL-2001; 2001US-0035841.
 XX 16-AUG-2001; 2001US-0035841.
 XX (GETH) GENENTECH INC.
 XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 XX Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-341962/32.
 XX N-PSDB; ACA06172.
 XX Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,
 XX PRO1887, PRO1785, PRO4333, useful for treating sports injuries,
 XX arthritis, diabetes, obesity, hyper- or hypo-insulinaemia.

PS Claim 12; Fig 34; 194pp; English.
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful in diagnosing or treating
 CC various bone and/or cartilage disorders (e.g. sports injuries,
 CC arthritis), various insulin deficient states (e.g. diabetes mellitus,
 CC hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated
 CC disorders (e.g. thalassaemia), kidney disorders associated with
 CC decreased mesangial cell function (e.g. Berger disease), or other
 CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
 CC dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide
 CC sequences may be used as hybridisation probes in chromosome and gene
 CC mapping, or in generating antisense RNA and DNA. They are also useful in
 CC preparing PRO polypeptides, in assays to identify other proteins or
 CC molecules involved in binding reaction, to generate transgenic animals or
 CC knockout animals, which in turn are useful in the development and
 CC screening of therapeutically useful reagents, for chromosome
 CC identification, and tissue typing. The PRO polypeptides and nucleic acid
 CC molecules are also useful in gene therapy, and as molecular weight
 CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
 CC used in diagnostic assays for PRO polypeptides, or for the affinity
 CC purification of the polypeptides from recombinant cell culture or natural
 CC sources. AB069103-AB069125 represent the human PRO polypeptides of the
 CC invention.
 XX Sequence 136 AA;
 SQ
 Query Match 99.3%; Score 136; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPTGPEPLVLLLLLAGAPAAAPTPTCTYSRMALSQEITRDNLNQVSESPFCVRYLPR 60
 DB 1 MPTGPEPLVLLLLLAGAPAAAPTPTCTYSRMALSQEITRDNLNQVSESPFCVRYLPR 60
 QY 61 LYLDIHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTTMNSFCRDLVFLDDCNA 120
 DB 61 LYLDIHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTTMNSFCRDLVFLDDCNA 120
 QY 121 LEYPIPTVTLVDRQR 136
 DB 121 LEYPIPTVTLVDRQR 136
 RESULT 7
 AB019435
 ID AB019435 standard; protein; 136 AA.
 XX AC AB019435;
 XX 27-AUG-2003 (first entry)
 XX Human secreted / transmembrane polypeptide PRO4425.
 XX Human; gene therapy; diabetes; obesity; hypoinsulinaemia.
 XX Homo sapiens.
 XX US2003027249-A1.
 XX 06-FEB-2003.
 XX 16-AUG-2001; 2001US-00931836.
 XX 15-MAY-1998; 98US-0085579P.
 XX 15-DEC-1998; 98US-0112514P.
 XX 22-DEC-1998; 98US-0113300P.
 XX 23-DEC-1998; 98US-0113430P.
 XX 23-DEC-1998; 98US-0113605P.
 XX 23-DEC-1998; 98US-0113821P.
 XX 23-DEC-1998; 98US-0114440P.

Db 61 LYLDHNYCVLDKLRDFVAPPCWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
QY 121 LEYPIPTVTLPPDROR 136
Db 121 LEYPIPTVTLPPDROR 136
RESULT 9
ID ABR39861 standard; protein; 136 AA.
XX ABR39861;
XX 11-AUG-2003 (first entry)
XX Human HEMAE80 polypeptide.
XX HEMAE80; bone resorption; osteopathic; bone deposition; human.
XX Homo sapiens.
XX WC2003014702-A2.
XX 20-FEB-2003.
XX 06-AUG-2002; 2002WO-US025068.
XX 08-AUG-2001; 2001US-0311027P.
XX (SCHE) SCHERING CORP.
XX Bazan JF, Beebe AM, De Waal Malefyt R, Gorman DM, Kirk P;
XX Kurata H, Rennick D;
XX WPI; 2003-256618/25.
XX N-PSDB; ACC47319.
XX Modulating bone resorption or treating bone resorption disorder, e.g.
XX osteoporosis, osteopetrosis, Paget's disease, osteodystrophy or Van
XX Buchem's disease, comprises administering a HEMAE80 agonist or
XX antagonist.
XX Claim 2; Page 23-24; 27pp; English.
XX The invention relates to modulating bone resorption or treating bone
XX resorption disorder and involves contacting a cell or administering a
XX HEMAE80 agonist or antagonist. The HEMAE80 antagonist is useful for
XX preventing loss of bone mineral density and for treating bone resorption
XX disorders such as osteoporosis, osteopetrosis, Paget's disease,
XX osteodystrophy, a result of a haemopoietic stem/progenitor hyperplasia,
XX or a result of an immune disorder or cancer. HEMAE80 agonists are useful
XX for inhibiting bone deposition and for treating excessive ossification of
XX skeletal bone, ossification of cartilage, or Van Buchem's disease.
XX HEMAE80 may be used to reduce bone mineral density. The present sequence
XX represents a human HEMAE80 polypeptide
XX Sequence 136 AA;
Query Match 99.3%; Score 136; DB 6; Length 136;
Best Local Similarity 100.0%; Pred. No. 8.9e-121;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRTGGLPVLVLLLAGAPAAATPTTCYGRMALSQEITRDNFLQVSPSPCVRYLPR 60
Db 1 MRTGGLPVLVLLLAGAPAAATPTTCYGRMALSQEITRDNFLQVSPSPCVRYLPR 60
QY 61 LYLDHNYCVLDKLRDFVAPPCWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
Db 61 LYLDHNYCVLDKLRDFVAPPCWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
QY 121 LEYPIPTVTLPPDROR 136
Db 121 LEYPIPTVTLPPDROR 136

Db 121 LEYPIPTVTLPPDROR 136
RESULT 10
ID ABU69096 standard; protein; 136 AA.
XX ABU69096;
XX AC ABU69096;
XX 02-JUN-2003 (first entry)
XX Human PRO polypeptide #17.
XX Human; PRO polypeptide; secreted and transmembrane protein; cancer;
XX non-insulin dependent diabetes mellitus; septic shock; stroke;
XX rheumatoid arthritis; graft-versus-host disease; cardiac ischaemia;
XX psoriasis; inflammatory bowel disease; asthma; antidiabetic; cytostatic;
XX immunosuppressive; antirheumatic; antiarthritic; cerebroprotective;
XX vasotropic; antipsoriatic; antiinflammatory; antiasthmatic.
XX Homo sapiens.
XX OS
XX US2003008348-A1.
XX 09-JAN-2003.
XX 26-DEC-2001; 2001US-00035855.
XX 15-MAY-1998; 98US-0085579P.
XX 15-DEC-1998; 98US-0112514P.
XX 22-DEC-1998; 98US-0113300P.
XX 23-DEC-1998; 98US-0113430P.
XX 23-DEC-1998; 98US-0113605P.
XX 23-DEC-1998; 98US-0113621P.
XX 23-DEC-1998; 98US-0114140P.
XX 12-JAN-1999; 99US-0115552P.
XX 22-JAN-1999; 99US-0116843P.
XX 23-MAR-1999; 99US-0125774P.
XX 23-MAR-1999; 99US-0125778P.
XX 24-MAR-1999; 99US-0125826P.
XX 31-MAR-1999; 99US-0127035P.
XX 05-APR-1999; 99US-0127706P.
XX 13-APR-1999; 99US-0129122P.
XX 21-APR-1999; 99US-0130359P.
XX 27-APR-1999; 99US-0131270P.
XX 27-APR-1999; 99US-0131272P.
XX 27-APR-1999; 99US-0131291P.
XX 04-MAY-1999; 99US-0132371P.
XX 04-MAY-1999; 99US-0132379P.
XX 04-MAY-1999; 99US-0132383P.
XX 14-MAY-1999; 99US-0132383P.
XX 25-MAY-1999; 99US-0132383P.
XX 08-JUN-1999; 99US-0138166P.
XX 20-JUL-1999; 99US-0144791P.
XX 03-AUG-1999; 99US-0146970P.
XX 29-OCT-1999; 99US-0162506P.
XX 02-DEC-1999; 99US-0162506P.
XX 22-DEC-1999; 99US-0162506P.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 22-MAY-2000; 2000WO-US014042.
XX 02-JUN-2000; 2000WO-US015264.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023522.
XX 01-DEC-2000; 2000WO-US032678.
XX 28-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-JUL-2001; 2001WO-US021735.
XX 16-AUG-2001; 2001US-00931836.
XX

PA (GETH) GENENTECH INC.
 XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-341326/32.
 DR N-PSDB; ACA06115.
 XX New PRO polypeptides and nucleic acid molecules, useful for diagnosing or
 PT treating diabetes mellitus, cancers, septic shock, inflammatory bowel
 PT disease or asthma, or in gene therapy, chromosome identification or
 PT tissue typing.
 XX Claim 12; Fig 34; 196pp; English.
 PS The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful in diagnosing or treating non
 CC -insulin dependent diabetes mellitus, cancers, septic shock, rheumatoid
 CC arthritis, graft-versus-host disease, stroke, cardiac ischaemia,
 CC psoriasis, inflammatory bowel disease or asthma. The PRO polynucleotide
 CC sequences may be used as hybridisation probes in chromosome and gene
 CC mapping, or in generating antisense RNA and DNA. They are also useful in
 CC preparing PRO polypeptides, in assays to identify other proteins or
 CC molecules involved in binding reaction, to generate transgenic animals or
 CC knockout animals, which in turn are useful in the development and
 CC screening of therapeutically useful reagents, for chromosome
 CC identification, and tissue typing. The PRO polypeptides and nucleic acid
 CC molecules are also useful in gene therapy, and as molecular weight
 CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
 CC used in diagnostic assays for PRO polypeptides, or for the affinity
 CC purification of the polypeptides from recombinant cell culture or natural
 CC sources. ABU69080-ABU69102 represent the human PRO polypeptides of the
 CC invention
 XX SQ Sequence 136 AA;
 Query Match 99.3%; Score 136; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121; Indels 0; Gaps 0;
 Matches 136; Conservative 0; Mismatches 0;
 QY 1 MRTGGLPVLLLLAGAPAAAPTPTCTCYSRMGALSQETITDFNLLQVSEPEPCVRYLPR 60
 Db 1 MRTGGLPVLLLLAGAPAAAPTPTCTCYSRMGALSQETITDFNLLQVSEPEPCVRYLPR 60
 QY 61 LYLDHNNYCVLDKLDKDFVASPCWKVAQVDSLKDKARKLYTITMNSFCRRDLVFLDDCNA 120
 Db 61 LYLDHNNYCVLDKLDKDFVASPCWKVAQVDSLKDKARKLYTITMNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPTVTTLVLPDRQR 136
 Db 121 LEYPIPTVTTLVLPDRQR 136
 RESULT 11
 ABU81560
 ID ABU81560 standard; protein; 136 AA.
 XX AC ABU81560;
 XX 24-JUN-2003 (first entry)
 XX Human secreted polypeptide PRO4425.
 KW Human; inflammatory disease; organ failure; atherosclerosis; cancer;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW differentiation disorder; cell adhesion disorder; skin disorder;
 KW neural receptor disorder; diabetic complication; tissue typing.
 XX OS Homo sapiens.
 XX US2002192751-A1.
 FN

XX 19-DEC-2002.
 PD 26-DEC-2001; 2001US-00036041.
 XX 15-MAY-1998; 98US-0085579P.
 PR 15-DEC-1998; 98US-0112514P.
 PR 22-DEC-1998; 98US-0113300P.
 PR 23-DEC-1998; 98US-0113430P.
 PR 23-DEC-1998; 98US-0113605P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 23-DEC-1998; 98US-0114140P.
 PR 12-JAN-1999; 99US-0115552P.
 PR 22-JAN-1999; 99US-0116843P.
 PR 23-MAR-1999; 99US-0125774P.
 PR 23-MAR-1999; 99US-0125778P.
 PR 31-MAR-1999; 99US-0125826P.
 PR 05-APR-1999; 99US-0127035P.
 PR 13-APR-1999; 99US-012706P.
 PR 21-APR-1999; 99US-0129122P.
 PR 27-APR-1999; 99US-0130359P.
 PR 27-APR-1999; 99US-0131270P.
 PR 27-APR-1999; 99US-0131291P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 04-MAY-1999; 99US-0132379P.
 PR 04-MAY-1999; 99US-0132383P.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-MAY-1999; 99US-0135750P.
 PR 08-JUN-1999; 99US-0138166P.
 PR 20-JUL-1999; 99US-0144791P.
 PR 03-AUG-1999; 99US-0146970P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99WO-US028551.
 PR 22-DEC-1999; 99WO-US030720.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019892.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 16-AUG-2001; 2001US-00931836.
 XX (GETH) GENENTECH INC.
 PA Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-341079/32.
 DR N-PSDB; ACA67738.
 XX New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
 PT cancer.
 XX Claim 12; Fig 34; 195pp; English.
 PS The invention relates to an isolated nucleic acid that encodes a PRO
 CC polypeptide. The nucleic acids and polypeptides are useful for treating
 CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
 CC infertility, birth defects, premature aging, acquired immunodeficiency
 CC syndrome (AIDS), cancer, differentiation disorders, cell adhesion
 CC disorders, neural receptor disorders, skin disorders or diabetic
 CC complications. The nucleic acids are useful as hybridisation probes, in
 CC chromosome and gene mapping and in generating antisense RNA or DNA. The

CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
 CC bioreactors. Both are useful in tissue typing. The present sequence
 CC represents the amino acid sequence of a PRO polypeptide of the invention
 XX
 SQ Sequence 136 AA;

Query Match 99.3%; Score 136; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRTGGLPVLLLLAGAPAAAPTPTTCYSRMALSQEITRDNLLQVSEPCVRYLPR 60
 Db 1 MRTGGLPVLLLLAGAPAAAPTPTTCYSRMALSQEITRDNLLQVSEPCVRYLPR 60
 Qy 61 LYLDHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTINMFCRDLVFLDDCNA 120
 Db 61 LYLDHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTINMFCRDLVFLDDCNA 120
 Qy 121 LEYPIPTVTLDPDRQR 136
 Db 121 LEYPIPTVTLDPDRQR 136

RESULT 12

ADA76590
 ID ADA76590 standard; protein; 136 AA.

AC ADA76590;

DT 20-NOV-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO4425.

XX human; secreted and transmembrane protein; PRO; tumour; gene therapy;
 XX tissue typing; chromosome identification; cytostatic.

OS Homo sapiens.

XX US2003036114-A1.

XX 20-FEB-2003.

XX 26-DEC-2001; 2001US-00035719.

XX 15-MAY-1998; 98US-0085579P.

XX 15-DEC-1998; 98US-0112514P.

XX 22-DEC-1998; 98US-0113300P.

XX 23-DEC-1998; 98US-0113430P.

XX 23-DEC-1998; 98US-0113605P.

XX 23-DEC-1998; 98US-0113621P.

XX 23-DEC-1998; 98US-0114140P.

XX 12-JAN-1999; 99US-0115552P.

XX 22-JAN-1999; 99US-0116843P.

XX 23-MAR-1999; 99US-0125774P.

XX 23-MAR-1999; 99US-0125778P.

XX 24-MAR-1999; 99US-0125826P.

XX 31-MAR-1999; 99US-0127035P.

XX 05-APR-1999; 99US-0127706P.

XX 13-APR-1999; 99US-0129122P.

XX 21-APR-1999; 99US-0130359P.

XX 27-APR-1999; 99US-0131270P.

XX 27-APR-1999; 99US-0131272P.

XX 27-APR-1999; 99US-0131291P.

XX 04-MAY-1999; 99US-0132371P.

XX 04-MAY-1999; 99US-0132379P.

XX 04-MAY-1999; 99US-0132383P.

XX 14-MAY-1999; 99US-0135750P.

XX 25-MAY-1999; 99US-0135750P.

XX 08-JUN-1999; 99US-0138166P.

XX 20-JUL-1999; 99US-0144791P.

XX 03-AUG-1999; 99US-0146970P.

XX 29-OCT-1999; 99US-0162506P.

XX 02-DEC-1999; 99US-0162551.

PR 22-DEC-1999; 99WO-US030720.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021866.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 16-AUG-2001; 2001US-00931836.
 XX
 XX (GETH) GENENTECH INC.

Deanoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 Stewart TA, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-615764/58.
 N-PSDB; ADA76589.

Novel isolated secreted and transmembrane polypeptides, designated as PRO
 polypeptides e.g. PRO484, PRO4334 and PRO1122, useful for inhibiting
 tumor cell growth, and for preparing medicaments for therapeutic use.

Claim 12; Fig 34; 201pp; English.

The invention describes an isolated secreted and transmembrane PRO
 polypeptide (I), having at least 80% identity to or scoring at least 80%
 positives when compared to, a sequence (SI) comprising 246, 440, 197, 97,
 273, 571, 209, 888, 502, 310, 251, 800, 507, 248, 223, 134, 136, 468,
 328, 221, 194, 899, or 339 amino acids fully defined in the
 specification. An anti-(I)-antibody is useful for determining the
 presence of (I) in a cell. (I) is useful for identifying a compound
 capable of inhibiting the expression and/or activity of (I). (I) and the
 antibody are useful for inhibiting the growth of tumour cells, and for
 the preparation of a medicament useful in the treatment of a condition
 which is responsive to (I) or the antibody. A polynucleotide (II)
 encoding (I) is also useful for isolating full-length PRO cDNA for
 generating transgenic animals or knock-out animals, which are, in turn,
 are useful in the development in the screening of therapeutically useful
 reagents, and in gene therapy. PRO is useful in assays to identify other
 proteins or molecules involved in binding interactions, for screening
 inhibitors or agonists of binding interactions and for screening chemical
 libraries. (I) is useful as molecular weight marker for protein
 electrophoresis, and as therapeutic agents. (I) or (II) is useful for
 tissue typing and for chromosome identification. Ab is useful in
 diagnostic assays for PRO, in affinity purification of PRO, and for
 detection of PRO in biological samples. This is the amino acid sequence
 of a novel human secreted and transmembrane PRO polypeptide.

Sequence 136 AA;

Query Match 99.3%; Score 136; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 8.9e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRTGGLPVLLLLAGAPAAAPTPTTCYSRMALSQEITRDNLLQVSEPCVRYLPR 60
 Db 1 MRTGGLPVLLLLAGAPAAAPTPTTCYSRMALSQEITRDNLLQVSEPCVRYLPR 60
 Qy 61 LYLDHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTINMFCRDLVFLDDCNA 120
 Db 61 LYLDHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTINMFCRDLVFLDDCNA 120
 Qy 121 LEYPIPTVTLDPDRQR 136
 Db 121 LEYPIPTVTLDPDRQR 136

PR	16-AUG-2001; 2001US-00931836.
XX	(GETH) GENENTECH INC.
XX	Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI	Stewart TA, Watanabe CK, Wood WL, Zhang Z;
XX	WPI; 2003-492260/46.
DR	N-FSDB; ACID42300.
XX	Novel secreted and transmembrane polypeptide for identifying agonists or
PT	antagonists of polypeptide, and as molecular weight markers.
XX	Claim 12; Fig 34; 195pp; English.
PS	The invention relates to an isolated, secreted and transmembrane
CC	polypeptide, termed PRO polypeptide, PRO having at least 80 % sequence
CC	identity to any one of the 23 100-900 residue amino acid sequences, given
CC	in the specification or to a sequence encoded by a nucleic acid molecule
CC	deposited under any one of the ATCC accession numbers given in the
CC	specification. Also included are an isolated nucleic acid molecule having
CC	at least 80 % sequence identity to any one of 23 400-3500 nucleotide
CC	sequences given in the specification, (or a nucleotide sequence encoding
CC	PRO, a full-length PRO coding sequence, a full-length coding sequence of
CC	DNA deposited under any ATCC accession number given in the specification)
CC	or at least 80 % identity to a nucleotide sequence encoding PRO, lacking
CC	its associated signal peptide, a sequence encoding extracellular domain
CC	of PRO with or without its associated signal peptide, a vector comprising
CC	the PRO nucleic acid, a host cell comprising the vector, preparation of
CC	PRO, a chimeric molecule comprising PRO fused to a heterologous amino
CC	acid sequence and an anti-PRO antibody. PRO is useful for identifying
CC	ant/agonists or antagonists of PRO, preparing a variant of PRO, as
CC	molecular weight markers and PRO nucleic acid is useful for recombinantly
CC	expressing those markers. PRO is also useful as therapeutic agent. PRO is
CC	useful in assays to identify molecules or proteins which bind to PRO and
CC	for identifying inhibitors of PRO. PRO nucleic acid is useful as a
CC	hybridisation probe, in chromosome and gene mapping, in generation of
CC	antisense RNA and DNA, for generating transgenic animals or knockout
CC	animals which in turn are useful in the development and screening of
CC	therapeutically useful reagents. PRO nucleic acid is also useful in
CC	mapping the gene which encodes the PRO and for the genetic analysis of
CC	individuals with genetic disorders, in gene therapy, for chromosome
CC	identification, as chromosome marker, and for generating probes for PCR,
CC	Northern analysis, Southern analysis and Western analysis. The antibody
CC	useful in diagnostic assays for PRO, for affinity purification of PRO,
CC	and for treating septic shock. PRO or the antibody is useful for the
CC	preparation of medicament for treating conditions which is responsive to
CC	the PRO polypeptide or anti-PRO antibody. PRO and PRO nucleic acid are
CC	useful for tissue typing. The present sequence represents a PRO protein
XX	Sequence 136 AA;
SQ	
Query Match	
Best Local Similarity 99.3%; Score 136; DB 7; Length 136;	
Matches 136, Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MRTGGLPVLLLLAGAPAAAPTPTTCYSRMRLSQEITRDFNLLQVSESPGPCRVILPR 60
Db	
1	MRTGGLPVLLLLAGAPAAAPTPTTCYSRMRLSQEITRDFNLLQVSESPGPCRVILPR 60
QY	61 LYLDIHNYCVLKLDRFVASPPCKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Db	
61	LYLDIHNYCVLKLDRFVASPPCKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
QY	121 LEYPIPVTTLVPDQR 136
Db	
121	LEYPIPVTTLVPDQR 136
RESULT 15	
AAE39113	
ID	AAE39113 standard; protein; 136 AA.
XX	

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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:09:18 ; Search time 23 Seconds
(without alignments)
307.511 Million cell updates/sec

Title: US-10-023-282-310
Perfect score: 137
Sequence: 1 MRTGFLPVLLLLAGAPAA.....CNALEYPIPVTVTLPRQRX 137

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.psp.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.psp.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.psp.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.psp.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.psp.*
6: /cgn2_6/ptodata/2/iaa/backfiles.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	99.3	137	4	US-08-205-258-310
2	8	5.8	30	3	US-08-448-489-7
3	8	5.8	54	1	US-08-464-339A-15
4	8	5.8	90	4	US-09-198-452A-1151
5	8	5.8	178	4	US-09-252-991A-20939
6	8	5.8	290	4	US-09-910-174B-19
7	8	5.8	290	4	US-09-620-461-19
8	8	5.8	319	4	US-09-910-174B-12
9	8	5.8	319	4	US-09-620-461-12
10	8	5.8	342	2	US-08-724-394A-6
11	8	5.8	350	4	US-09-651-200-25
12	8	5.8	350	4	US-09-910-174B-17
13	8	5.8	350	4	US-09-620-461-17
14	8	5.8	351	1	US-08-468-847B-16
15	8	5.8	357	4	US-09-910-174B-14
16	8	5.8	357	4	US-09-620-461-14
17	8	5.8	361	3	US-08-652-265-22
18	8	5.8	361	3	US-08-834-497A-22
19	8	5.8	361	3	US-09-503-444A-22
20	8	5.8	447	4	US-09-489-039A-11893
21	8	5.8	474	4	US-09-252-991A-29269
22	8	5.8	513	4	US-09-910-174B-18
23	8	5.8	513	4	US-09-620-461-18
24	8	5.8	540	2	US-08-724-394A-4
25	8	5.8	573	3	US-08-704-711A-1
26	8	5.8	579	4	US-09-521-220-1
27	8	5.8	582	3	US-08-704-711A-2

ALIGNMENTS

RESULT 1

US-09-205-258-310
; Sequence 310, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

Sequence 1, Appli
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Sequence 2, Appli
Sequence 28, Appli
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Sequence 187, App
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Sequence 187, App
Sequence 187, App
Sequence 28, Appli
Sequence 624, App
Sequence 50, Appli
Sequence 15, Appli

28 8 5.8 582 3 US-08-448-489-1
29 8 5.8 582 3 US-09-211-704A-9
30 8 5.8 582 4 US-09-521-220-2
31 8 5.8 582 4 US-09-391-104-28
32 8 5.8 4563 4 US-09-108-006C-1
33 7 5.1 9 1 US-08-462-128-28
34 7 5.1 9 1 US-08-463-180-28
35 7 5.1 18 3 US-08-469-318-187
36 7 5.1 18 3 US-08-468-609A-187
37 7 5.1 18 3 US-08-875-533-28
38 7 5.1 18 4 US-08-446-872A-187
39 7 5.1 18 4 US-08-762-227A-187
40 7 5.1 18 5 PCT-US95-01185-187
41 7 5.1 28 1 US-08-164-151-22
42 7 5.1 32 1 US-07-662-005A-8
43 7 5.1 34 4 US-09-149-476-624
44 7 5.1 57 2 US-08-318-837-50
45 7 5.1 57 4 US-09-235-451-15

EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 310
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (137)
OTHER INFORMATION: Xaa equals stop translation

Query Match 99.3%; Score 136; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 2e-120;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTGGLPVLLLLAGAAAPTPTCTYSRRAISQETTRDFNLLQVSEPCVRYLPR 60
DB 1 MRTGGLPVLLLLAGAAAPTPTCTYSRRAISQETTRDFNLLQVSEPCVRYLPR 60
QY 61 LYLDHNYCVLDKLRDFVSPPCWKAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
DB 61 LYLDHNYCVLDKLRDFVSPPCWKAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
QY 121 LEYPIPTVTVLPDQR 136
DB 121 LEYPIPTVTVLPDQR 136

RESULT 2
US-08-448-489-7
; Sequence 7, Application US/08448489
; Patent No. 6184022

GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-08-448-489-7

Query Match 5.8%; Score 8; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
DB 12 LPVLLLLL 19

RESULT 3
US-08-464-339A-15
; Sequence 15, Application US/08464339A
; Patent No. 5747280
GENERAL INFORMATION:
APPLICANT: HASTINGS, ET AL.
TITLE OF INVENTION: Human Vascular IBP-Like Growth
TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM.
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,339A
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14388
FILING DATE: 9 DEC 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-332
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-464-339A-15

Query Match 5.8%; Score 8; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
| | | | |
Db 9 LPVLLLLL 16

RESULT 4

US-09-198-452A-1151
; Sequence 1151, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffiths, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 1151

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-1151

Query Match 5.8%; Score 8; DB 4; Length 90;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VLLLLLAG 16
| | | | |
Db 37 VLLLLLAG 44

RESULT 5

US-09-252-991A-20939

; Sequence 20939, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 20939

; LENGTH: 178

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20939

Query Match 5.8%; Score 8; DB 4; Length 178;

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLLAG 17
| | | | |
Db 74 LLLLLLAG 81

RESULT 6

US-09-910-174B-19

; Sequence 19, Application US/09910174B

; Patent No. 6630575

; GENERAL INFORMATION:

; APPLICANT: Coyle, Anthony J.

; APPLICANT: Fraser, Christopher C.

; APPLICANT: Manning, Stephen

; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7

; FILE REFERENCE: 35800/236924

; CURRENT APPLICATION NUMBER: US/09/910,174B

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/620,461

; PRIOR FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 290

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-910-174B-19

Query Match 5.8%; Score 8; DB 4; Length 290;

Best Local Similarity 100.0%; Pred. No. 9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
| | | | |
Db 254 LPVLLLLL 261

RESULT 7

US-09-620-461-19

; Sequence 19, Application US/09620461

; Patent No. 6635750

; GENERAL INFORMATION:

; APPLICANT: Coyle, Anthony J.

; APPLICANT: Fraser, Christopher C.

; APPLICANT: Manning, Stephen

; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7

; TITLE OF INVENTION: Family and Uses Thereof

; FILE REFERENCE: 5800-149

; CURRENT APPLICATION NUMBER: US/09/620,461

; CURRENT FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 19

; LENGTH: 290

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-620-461-19

Query Match 5.8%; Score 8; DB 4; Length 290;

Best Local Similarity 100.0%; Pred. No. 9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
| | | | |
Db 254 LPVLLLLL 261

RESULT 8

US-09-910-174B-12

; Sequence 12, Application US/09910174B

; Patent No. 6630575

; GENERAL INFORMATION:

; APPLICANT: Coyle, Anthony J.

; APPLICANT: Fraser, Christopher C.

; APPLICANT: Manning, Stephen

; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7

; TITLE OF INVENTION: Family and Uses Thereof

; FILE REFERENCE: 35800/236924

; CURRENT APPLICATION NUMBER: US/09/910,174B

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/620,461

; PRIOR FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 319

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-12

Query Match          5.8%; Score 8; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LLLLLLAGA 17
Db 259 LLLLLLAGA 266

RESULT 9
US-09-620-461-12
; Sequence 12, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-12

Query Match          5.8%; Score 8; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LLLLLLAGA 17
Db 259 LLLLLLAGA 266

RESULT 10
US-08-724-394A-6
; Sequence 6, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..342
; OTHER INFORMATION: /note= "BTF4"
US-08-724-394A-6

Query Match          5.8%; Score 8; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LLLLLLAGA 17
Db 275 LLLLLLAGA 282

RESULT 11
US-09-651-200-25
; Sequence 25, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-651-200-25

Query Match          5.8%; Score 8; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVLLLLLL 14
Db 254 LPVLLLLLL 261

RESULT 12
US-09-910-174B-17
; Sequence 17, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
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; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-17

Query Match          5.8%; Score 8; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
Db 254 LPVLLLLL 261

RESULT 13
US-09-620-461-17
; Sequence 17, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-17

Query Match          5.8%; Score 8; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
Db 254 LPVLLLLL 261

RESULT 14
US-08-468-847B-16
; Sequence 16, Application US/08468847B
; Patent No. 5780263
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
; TITLE OF INVENTION: Human CGN-Like Growth Factor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,847B
; FILING DATE: 6 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-468-847B-16

Query Match          5.8%; Score 8; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
Db 9 LPVLLLLL 16

RESULT 15
US-09-910-174B-14
; Sequence 14, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-14

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Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 257 LLLLLL 264

Search completed: February 25, 2004, 05:12:52
Job time : 25 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:11:28 ; Search time 34 Seconds

(without alignments)
850.823 Million cell updates/sec

Title: US-10-023-282-310

Perfect score: 137

Sequence: 1 MRTPGFLPVLLLLAGAPAA.....CNALEYPIPTVTVLPRQRX 137

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	136	99.3	136	13	US-10-036-342-65
3	136	99.3	136	13	US-10-036-041-65
4	136	99.3	136	14	US-10-036-855-65
5	136	99.3	136	14	US-10-036-214-65
6	136	99.3	136	14	US-10-035-719-65
7	136	99.3	136	14	US-10-036-160-65
8	136	99.3	136	14	US-10-020-419-2
9	136	99.3	136	14	US-10-035-958-65
10	136	99.3	136	14	US-10-036-150-65
11	136	99.3	136	14	US-10-213-288-2
12	136	99.3	136	14	US-10-036-063-65
13	136	99.3	136	14	US-10-223-085-312
14	136	99.3	136	14	US-10-223-084-312
15	136	99.3	136	14	US-10-223-088-312

16	136	99.3	136	14	US-10-223-090-312	Sequence 312, App
17	136	99.3	136	14	US-10-223-087-312	Sequence 312, App
18	136	99.3	136	14	US-10-223-083-312	Sequence 312, App
19	136	99.3	136	14	US-10-223-089-312	Sequence 312, App
20	136	99.3	136	14	US-10-035-977-65	Sequence 65, Appl
21	136	99.3	136	14	US-10-223-081-312	Sequence 312, App
22	136	99.3	136	14	US-10-223-082-312	Sequence 312, App
23	136	99.3	137	10	US-09-933-767-310	Sequence 310, App
24	136	99.3	137	14	US-10-023-282-310	Sequence 310, App
25	112	81.8	112	10	US-09-933-767-1245	Sequence 1245, Ap
26	18	13.1	136	14	US-10-020-419-4	Sequence 4, Appli
27	18	13.1	139	14	US-10-213-288-4	Sequence 4, Appli
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29	8	5.8	90	15	US-10-289-762-1151	Sequence 1151, Ap
30	8	5.8	131	14	US-10-097-065-442	Sequence 442, App
31	8	5.8	136	14	US-10-156-761-7843	Sequence 7843, Ap
32	8	5.8	240	15	US-10-093-463-164	Sequence 164, App
33	8	5.8	261	14	US-10-245-103-86	Sequence 86, Appl
34	8	5.8	261	14	US-10-245-107-86	Sequence 86, Appl
35	8	5.8	261	14	US-10-245-143-86	Sequence 86, Appl
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39	8	5.8	261	14	US-10-237-535-86	Sequence 86, Appl
40	8	5.8	261	14	US-10-238-183-86	Sequence 86, Appl
41	8	5.8	261	14	US-10-238-283-86	Sequence 86, Appl
42	8	5.8	261	14	US-10-238-370-86	Sequence 86, Appl
43	8	5.8	261	14	US-10-245-055-86	Sequence 86, Appl
44	8	5.8	261	14	US-10-245-147-86	Sequence 86, Appl
45	8	5.8	261	14	US-10-245-730-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1

US-09-931-836-65

; Sequence 65, Application US/09931836

; Publication No. US20030027249A1

; GENERAL INFORMATION:

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3030R1C1

; CURRENT APPLICATION NUMBER: US/09/931,836

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/085579

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/112514

; PRIOR FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: 60/113300

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: 60/113430

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/113605

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/114140

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/115552

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/116843

; PRIOR FILING DATE: 1999-01-22

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; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
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; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
US-03-931-836-65

Query Match 99.3%; Score 136; DB 10; Length 136;

Best Local Similarity 100.0%; Pred. No. 7.8e-115;

Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRTEGPLEVLLLAGAPAAAPTPTCTCYSRMALSOETTRDFNLLQVSEPCVRYLPR 60
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Qy 121 LEYDIPVTTVLPDRQR 136
Db 121 LEYDIPVTTVLPDRQR 136

RESULT 2

US-10-036-342-65
; Sequence 65, Application US/10036342
; Publication No. US20020090681A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C5
; CURRENT APPLICATION NUMBER: US/10/036,342
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 09/874503
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908, 827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
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; PRIOR APPLICATION NUMBER: PCT/US99/28551
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; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: 2000-03-02
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; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-041-65

Query Match 99.3%; Score 136; DB 13; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.9e-115;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-10-035-855-65
; Sequence 65, Application US/10035855
; Publication No. US20030008348A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P1030R1C4
; CURRENT APPLICATION NUMBER: US/10/035,855
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
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PRIOR APPLICATION NUMBER: 09/380142
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PRIOR FILING DATE: 2000-12-20
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PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
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PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 65
LENGTH: 136
TYPE: PRT
ORGANISM: Homo Sapien
US-10-035-855-65

Query Match 99.3%; Score 136; DB 14; Length 136;

Best Local Similarity 100.0%; Pred. No. 7.8e-115; Indels 0; Gaps 0;
Matches 136; Conservative 0; Mismatches 0;

Qy	1	MRTFGPLPVLILLAGAPAAARPTPTCYSGMRALSQETITRDFNLLQVSESEPCVRYLPR	60
Db	1	MRTFGPLPVLILLAGAPAAARPTPTCYSGMRALSQETITRDFNLLQVSESEPCVRYLPR	60
Qy	61	LYLDHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA	120
Db	61	LYLDHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA	120
Qy	121	LEYPIPVTTVLPRQR	136
Db	121	LEYPIPVTTVLPRQR	136

RESULT 5

US-10-036-214-65
Sequence 65, Application US/10036214
Publication No. US20030032061A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C11
CURRENT APPLICATION NUMBER: US/10/036,214
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
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; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
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; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
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; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
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; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
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; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733

; PRIOR FILING DATE: 1999-05-14
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
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; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
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; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
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; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-214-65

Query Match 99.3%; Score 136; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.8e-115; Mismatches 0; Indels 0; Gaps 0;

Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRTEGPIPLVLLLAGAPAAARPTPTCYSRMRALSQBITRDNLLQVSESEPCVRYLPR 60
Db 1 MRTEGPIPLVLLLAGAPAAARPTPTCYSRMRALSQBITRDNLLQVSESEPCVRYLPR 60
Qy 61 LYLDHNYCVLDKLRDFVAPPCWKVAQVSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Db 61 LYLDHNYCVLDKLRDFVAPPCWKVAQVSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Qy 121 LEYPIPTVTVLPDRQR 136
Db 121 LEYPIPTVTVLPDRQR 136

RESULT 6

US-10-035-719-65
; Sequence 65, Application US/10035719
; Publication No. US20030036114A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C2

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C3
CURRENT APPLICATION NUMBER: US/10/036,160
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
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PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
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PRIOR APPLICATION NUMBER: 60/125774
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PRIOR APPLICATION NUMBER: 60/125826
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PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/132379
PRIOR FILING DATE: 1999-05-04
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PRIOR FILING DATE: 1999-05-04
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PRIOR APPLICATION NUMBER: 60/138166
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PRIOR APPLICATION NUMBER: 60/146970
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PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280

PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
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PRIOR FILING DATE: 2000-08-24
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PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
SEQ ID NO 65
LENGTH: 136
TYPE: PRT
ORGANISM: Homo Sapien
US-10-036-160-65
Query Match 99.3%; Score 136; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.8e-115;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRTGPIPVLLILLAGAPAAAPTPTCTYSRMRALSQEITRDENLLOYSEPEPCVRYLPR 60
DB 1 MRTGPIPVLLILLAGAPAAAPTPTCTYSRMRALSQEITRDENLLOYSEPEPCVRYLPR 60
QY 61 LYLDIHNVCVLDKLRDFVSPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
DB 61 LYLDIHNVCVLDKLRDFVSPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
QY 121 LEYPIPVTTVLPDRQR 136
DB 121 LEYPIPVTTVLPDRQR 136
RESULT 8
US-10-020-419-2
Sequence 2, Application US/10020419
Publication No. US20030044897A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
APPLICANT: Ye, Weilan
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: NOVEL SECRETED POLYPEPTIDE AND METHODS OF TREATMENT OF


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; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-035-958-65

Query Match      99.3%; Score 136; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.8e-115;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTGPELVILLLAGAPAAARPTPTCYSRMRALSQEITRDNFLNQVSEPSPCVRYLPR 60
Db 1 MRTGPELVILLLAGAPAAARPTPTCYSRMRALSQEITRDNFLNQVSEPSPCVRYLPR 60

Qy 61 LYLDHNYCVLDKRDVFASPPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Db 61 LYLDHNYCVLDKRDVFASPPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120

Qy 121 LEYPIPTVTLVDRQR 136
Db 121 LEYPIPTVTLVDRQR 136

RESULT 10
US-10-036-150-65
; Sequence 65, Application US/10036150
; Publication No. US20030949734A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C9
; CURRENT APPLICATION NUMBER: US/10/036,150
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140

; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
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; PRIOR APPLICATION NUMBER: 09/380142
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; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
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; PRIOR FILING DATE: 2000-03-01
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; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
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; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
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; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
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; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-150-65

Query Match          99.3%; Score 136; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.8e-115;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTGGLPVLLLLLAGAAPARPTPTCYSRMRALSOEITRDFNLLQVSESEPCVRYLPR 60
DB 1 MRTGGLPVLLLLLAGAAPARPTPTCYSRMRALSOEITRDFNLLQVSESEPCVRYLPR 60
QY 61 LYLDIHNVCVLDKLRDFVASPPCKVQAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
DB 61 LYLDIHNVCVLDKLRDFVASPPCKVQAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
QY 121 LEYPIPVTTVLPRQR 136
DB 121 LEYPIPVTTVLPRQR 136

RESULT 12
US-10-036-063-65
; Sequence 65, Application US/10036063
; Publication No. US20030092063A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C6
; CURRENT APPLICATION NUMBER: US/10/036,063
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
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; PRIOR APPLICATION NUMBER: 60/125774
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; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131272
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371

QY 1 MRTGGLPVLLLLLAGAAPARPTPTCYSRMRALSOEITRDFNLLQVSESEPCVRYLPR 60
DB 1 MRTGGLPVLLLLLAGAAPARPTPTCYSRMRALSOEITRDFNLLQVSESEPCVRYLPR 60
QY 61 LYLDIHNVCVLDKLRDFVASPPCKVQAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
DB 61 LYLDIHNVCVLDKLRDFVASPPCKVQAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
QY 121 LEYPIPVTTVLPRQR 136
DB 121 LEYPIPVTTVLPRQR 136

US-10-213-288-2
; Sequence 2, Application US/10213288
; Publication No. US20030082184A1
; GENERAL INFORMATION:
; APPLICANT: Bazan, Jose F.
; APPLICANT: Beebe, Amy M.
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kirk, Peter
; APPLICANT: Kurata, Hirokazu
; APPLICANT: Rennick, Donna
; TITLE OF INVENTION: USES OF MAMMALIAN CYTOKINE, RELATED REAGENTS
; FILE REFERENCE: DX01465X
; CURRENT APPLICATION NUMBER: US/10/213,288
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US 60/311,027
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-213-288-2

Query Match          99.3%; Score 136; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.8e-115;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/132379
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/132383
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138166
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/146970
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 65
LENGTH: 136
TYPE: PRT
ORGANISM: Homo Sapien
US-10-036-063-65

Query Match 99.3%; Score 136; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.8e-115; Indels 0; Gaps 0;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTGPLPVLVLLLAGAPAAAPTPTTCYSRMRALSQETTRDFNLLQVSEPCVRYLPR 60
DB 1 MRTGPLPVLVLLLAGAPAAAPTPTTCYSRMRALSQETTRDFNLLQVSEPCVRYLPR 60
QY 61 LYLDIHNVCVLDKURDFVSPCKWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
DB 61 LYLDIHNVCVLDKURDFVSPCKWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
QY 121 LEYPIPTVTVLPDRQR 136
DB 121 LEYPIPTVTVLPDRQR 136

RESULT 13

US-10-223-085-312
Sequence 312, Application US/10223085
Publication No. US20030100497A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PIC10
CURRENT APPLICATION NUMBER: US/10/223,085
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 312
LENGTH: 136
TYPE: PRT
ORGANISM: Homo sapiens
US-10-223-085-312

Query Match 99.3%; Score 136; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.8e-115;

us-10-023-282-310.rapb

Wed Feb 25 11:56:33 2004

Qy 61 LYLDIHNYCVLDKLRDFVASPPCKVAVQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Db 61 LYLDIHNYCVLDKLRDFVASPPCKVAVQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Qy 121 LEYPIPVTTVLPDROR 136
Db 121 LEYPIPVTTVLPDROR 136

Search completed: February 25, 2004, 05:17:14
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2004, 04:56:51 ; Search time 57 Seconds

(without alignments)
679.105 Million cell updates/sec

Title: US-10-023-282-310

Perfect score: BLOSUM62
Sequence: 1 MRPFGPLPVLILLAGAPAA.....CNALXPVPVTTLVLPDRQX 137

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	724	99.9	136	3 AAB18925	Aab18925 A novel p
2	724	99.9	136	3 AAB28612	Aab28612 Human C17
3	724	99.9	136	5 ABB84972	Abb84972 Human PRO
4	724	99.9	136	5 ABB95578	Abb95578 Human ang
5	724	99.9	136	6 ABP70605	Abp70605 Amino aci
6	724	99.9	136	6 ABU69119	Abu69119 Human PRO
7	724	99.9	136	6 ABO19435	Abo19435 Human sec
8	724	99.9	136	6 AAO16398	Aao16398 Human C17
9	724	99.9	136	6 ABR39861	Abr39861 Human HEM
10	724	99.9	136	6 ABU69096	Abu69096 Human PRO
11	724	99.9	136	6 ABU81560	Abu81560 Human sec
12	724	99.9	136	6 ADA76590	Ada76590 Novel hum
13	724	99.9	136	6 ABU08232	Abu08232 Human PRO
14	724	99.9	136	6 ABO25143	Abo25143 Human sec
15	724	99.9	136	7 AAE39113	Aae39113 Human PRO
16	724	99.9	136	7 AAE39050	Aae39050 Human PRO
17	724	99.9	136	7 ADC29821	Adc29821 Novel hum
18	724	99.9	136	7 ADD10601	Add10601 Human sec
19	724	99.9	136	7 ADD11561	Add11561 Human sec
20	724	99.9	136	7 ADD37354	Add37354 Human sec
21	724	99.9	136	8 ADE41562	Ade41562 Human sec
22	724	99.9	137	2 AAW88595	Aaw88595 Secreted
23	724	99.9	137	4 ABB50362	Abb50362 Human sec
24	724	99.9	137	6 ABO44619	Abo44619 Novel hum
25	724	99.9	137	7 ABO26099	Abo26099 Human pro

ALIGNMENTS

RESULT 1

AAB18925
ID AAB18925 standard; protein; 136 AA.

XX AAB18925;

XX AC

XX DT 08-FEB-2001 (first entry)

XX XX

DE A novel polypeptide designated PRO4425.

XX XX

XX KW Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
XX KW insulinemia; kidney disorder; Bergers disease; nephropathy;
XX KW Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
XX KW Crohns disease.

XX OS Homo sapiens.

XX XX

XX FH Key Location/Qualifiers

XX Peptide 1..19

XX FT Modified-site /note= "signal sequence"

XX FT Modified-site 16..22

XX FT Modified-site /note= "N-myristoylation site"

XX FT Modified-site 60..69

XX FT Modified-site /note= "tyrosine kinase phosphorylation site"

XX WO2000056889-A2.

XX 28-SEP-2000.

XX 01-MAR-2000; 2000WO-US0005601.

XX 23-MAR-1999; 99US-0125774P.

XX 23-MAR-1999; 99US-0125778P.

XX 24-MAR-1999; 99US-0125826P.

XX 31-MAR-1999; 99US-0127035P.

XX 05-APR-1999; 99US-0127706P.

XX 21-APR-1999; 99US-0130359P.

XX 27-APR-1999; 99US-0131270P.

XX 27-APR-1999; 99US-0131272P.

XX 27-APR-1999; 99US-0131291P.

XX 04-MAY-1999; 99US-0132371P.

XX 04-MAY-1999; 99US-0132379P.

XX 04-MAY-1999; 99US-0132383P.

XX 25-MAY-1999; 99US-0135750P.

XX 08-JUN-1999; 99US-0138166P.

Abb51287 Human sec
Aao16399 Bovine C1
Aao16400 Murine HE
Aab39862 Murine HE
Abp70606 Amino aci
Abu08233 Mouse pro
Adc31787 Human nov
Aab59415 Drosophila
Aaw46286 Human gra
Aau98084 Human SCY
Abu56721 Lung canc
Aab44247 Human wil
Aau33297 Novel hum
Aau02903 Angiotens
Aam40056 Human pol
Ada50545 Human fac
Aau11270 Human coa
Aab19104 Polypepti
Abg28780 Novel hum
Abp65007 Human pro

PF 20-JUN-2001; 2001WO-US019692.
 XX 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 28-JUL-2000; 2000US-0220664P.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-0222695P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023522.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-0230978P.
 PR 24-OCT-2000; 2000US-0242322P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00767609.
 PR 01-MAR-2001; 2001US-00806666.
 PR 09-MAR-2001; 2001US-00806666.
 PR 14-MAR-2001; 2001US-00806666.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX 01-JUN-2001; 2001WO-US017800.
 XX (GETH) GENENTECH INC.
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2002-090516/12.
 DR N-PSDB; ABL88227.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 11; Fig 312; 565pp; English.
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABL8817 to
 CC ABL885003. The PRO proteins and polynucleotides have cardiatic, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX SQ Sequence 136 AA;
 Query Match 99.9%; Score 724; DB 5; Length 136;
 Best Local Similarity 100.0%; Pred. NO. 1.2e-70;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 M R T P G L P V L L L L L L A G A P A A R P T P T C Y S R M R A L S Q E I T R D F N L L Q V S E S E C V R Y L P R 60
 DB 1 M R T P G L P V L L L L L L A G A P A A R P T P T C Y S R M R A L S Q E I T R D F N L L Q V S E S E C V R Y L P R 60
 QY 61 L Y L D I H N Y C V L D K I R D F V A S P P C W K V A Q V D S L K D K A R K L Y T I M N S F C R R D L V F L L D D C N A 120
 DB 61 L Y L D I H N Y C V L D K I R D F V A S P P C W K V A Q V D S L K D K A R K L Y T I M N S F C R R D L V F L L D D C N A 120
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 DB 121 L E Y P I P V T T V L P D R Q R 136
 RESULT 4
 ABB95578
 ID ABB95578 standard; protein; 136 AA.
 XX ABB95578;
 AC ABB95578;
 XX 19-JUL-2002 (first entry)
 DT Human angiogenesis related protein PRO4425 SEQ ID NO: 312.
 XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiant; cyrostatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.
 XX Homo sapiens.
 OS WC200208284-A2.
 PN 31-JAN-2002.
 XX 09-JUL-2001; 2001WO-US021735.
 XX 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 28-JUL-2000; 2000US-0220664P.
 PR 02-AUG-2000; 2000WO-US020710.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242322P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-0076498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 30-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX 20-JUN-2001; 2001WO-US019692.
 XX

PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GUEN/) GUENEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gueneay AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI: 2002-171999/22.
 DR N-PSDB; ABL95716.
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 312; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention
 XX
 SQ Sequence 136 AA;
 Query Match 99.9%; Score 724; DB 5; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.2e-70;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRTGGLPVLILLLAGAPAAAPTPTCTCYSRMRALSQETTRDFNLQVSESPPCVRYLPR 60
 DB 1 MRTGGLPVLILLLAGAPAAAPTPTCTCYSRMRALSQETTRDFNLQVSESPPCVRYLPR 60
 QY 61 LYLDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 DB 61 LYLDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPVTTVLPDRQR 136
 DB 121 LEYPIPVTTVLPDRQR 136
 RESULT 5
 ABP70605
 ID ABP70605 standard; protein; 136 AA.
 XX
 XX ABP70605;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Amino acid sequence of human secreted polypeptide designated PRO4425.
 XX
 KW Human; secreted polypeptide; PRO4425; bone disorder; osteoarthritis;
 KW bone damage; cartilage damage; osteoporosis; osteomyelitis;
 KW osteogenesis imperfecta; rheumatoid arthritis.
 XX
 XX Homo sapiens.11.
 OS

XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Modified-site /note= "signal peptide"
 FT Modified-site 16..22
 FT Modified-site /note= "N-myristoylation site"
 FT Modified-site 60..69
 FT Modified-site /note= "tyrosine kinase phosphorylation site"
 XX
 PN WO2003000729-A2.
 XX
 XX 03-JAN-2003.
 PD
 PD 13-DEC-2001; 2001WO-US048938.
 PF
 PF 20-JUN-2001; 2001WO-US019692.
 XX
 PR 09-JUL-2001; 2001WO-US021735.
 PR
 PA (GETH) GENENTECH INC.
 PI
 PI Goddard A, Wood WI, Ye W, Zhang Z;
 XX
 XX WPI: 2003-175282/17.
 DR N-PSDB; ABZ68432.
 DR
 XX New secreted nucleic acid encoding a polypeptide, designated PRO4425, for
 PT treating bone disorders, such as, osteoarthritis, damage through trauma,
 PT osteoporosis, osteomyelitis, osteogenesis imperfecta, or rheumatoid
 PT arthritis.
 XX
 PS Claim 10; Fig 2; 93pp; English.
 CC
 CC The present sequence represents a human secreted polypeptide, designated
 CC PRO4425. The polypeptide has a calculated molecular weight of 15577
 CC daltons, and a structure that is similar to the interleukin-8 family of
 CC proteins. The PRO4425 polynucleotide and polypeptide are useful for
 CC treating bone disorders, such as osteoarthritis, damage to the bone or
 CC cartilage through trauma, osteoporosis, osteomyelitis, osteogenesis
 CC imperfecta, or rheumatoid arthritis. The nucleic acids are useful as
 CC hybridization probes, in chromosome and gene mapping, and in generating
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. Both PRO4425 polynucleotide and
 CC polypeptide are useful in tissue typing
 XX
 SQ Sequence 136 AA;
 Query Match 99.9%; Score 724; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.2e-70;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRTGGLPVLILLLAGAPAAAPTPTCTCYSRMRALSQETTRDFNLQVSESPPCVRYLPR 60
 DB 1 MRTGGLPVLILLLAGAPAAAPTPTCTCYSRMRALSQETTRDFNLQVSESPPCVRYLPR 60
 QY 61 LYLDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 DB 61 LYLDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPVTTVLPDRQR 136
 DB 121 LEYPIPVTTVLPDRQR 136
 RESULT 6
 ABU69119
 ID ABU69119 standard; protein; 136 AA.
 XX
 XX ABU69119;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human PRO polypeptide #17.
 XX

KW Human; secreted and transmembrane protein; bone disorder; obesity;
 KW cartilage disorder; sports injury; arthritis; diabetes mellitus;
 KW hypo-insulinaemia; obesity; hyper-insulinaemia; chalaasaemia;
 KW haemoglobin-associated disorder; kidney disorder; Berger disease;
 KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;
 KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;
 KW antiarthritic; antidiabetic; antianaemic; nephrotropic; antiinflammatory.
 XX Homo sapiens.
 OS
 XX US2003032061-A1.
 XX 13-FEB-2003.
 XX 26-DEC-2001; 2001US-00036214.
 XX 15-MAY-1998; 98US-0085579P.
 XX 15-DEC-1998; 98US-0112514P.
 XX 23-DEC-1998; 98US-0113300P.
 XX 23-DEC-1998; 98US-0113430P.
 XX 23-DEC-1998; 98US-0113605P.
 XX 23-DEC-1998; 98US-0113621P.
 XX 23-DEC-1998; 98US-0114140P.
 XX 23-DEC-1998; 98US-0115552P.
 XX 23-MAR-1999; 99US-0116843P.
 XX 23-MAR-1999; 99US-0125774P.
 XX 23-MAR-1999; 99US-0125778P.
 XX 23-MAR-1999; 99US-0125826P.
 XX 31-MAR-1999; 99US-0127035P.
 XX 03-APR-1999; 99US-0127706P.
 XX 13-APR-1999; 99US-0129122P.
 XX 21-APR-1999; 99US-0130359P.
 XX 27-APR-1999; 99US-0131270P.
 XX 27-APR-1999; 99US-0131272P.
 XX 27-APR-1999; 99US-0131291P.
 XX 04-MAY-1999; 99US-0132371P.
 XX 04-MAY-1999; 99US-0132379P.
 XX 04-MAY-1999; 99US-0132383P.
 XX 14-MAY-1999; 99US-0132383P.
 XX 24-MAY-1999; 99US-0135750P.
 XX 08-JUN-1999; 99US-0138166P.
 XX 20-JUL-1999; 99US-0144791P.
 XX 03-AUG-1999; 99US-0146970P.
 XX 28-OCT-1999; 99US-0162506P.
 XX 02-DEC-1999; 99US-0208551P.
 XX 22-DEC-1999; 99US-0208551P.
 XX 01-MAR-2000; 2000WO-US030720.
 XX 02-MAR-2000; 2000WO-US005601.
 XX 22-MAY-2000; 2000WO-US005841.
 XX 02-JUN-2000; 2000WO-US014042.
 XX 23-AUG-2000; 2000WO-US015264.
 XX 24-AUG-2000; 2000WO-US023522.
 XX 01-DEC-2000; 2000WO-US023328.
 XX 28-DEC-2000; 2000WO-US032578.
 XX 28-FEB-2001; 2001WO-US006520.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 20-JUN-2001; 2001WO-US019692.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-JUL-2001; 2001WO-US021735.
 XX 16-AUG-2001; 2001US-00931836.
 XX (GETH) GENENTECH INC.
 XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CX, Wood WI, Zhang Z;
 XX WPI; 2003-341962/32.
 XX N-PSDB; ACA06172.
 XX Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,
 PT PRO1887, PRO1785, PRO4353 useful for treating sports injuries,
 PT arthritis, diabetes, obesity, hyper- or hypo-insulinemia.
 XX

PS Claim 12; Fig 34; 194pp; English.
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful in diagnosing or treating
 CC various bone and/or cartilage disorders (e.g. sports injuries,
 CC arthritis), various insulin deficient states (e.g. diabetes mellitus,
 CC hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated
 CC disorders (e.g. thalassaemia), kidney disorders associated with
 CC decreased mesangial cell function (e.g. Berger disease), or other
 CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
 CC dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide
 CC sequences may be used as hybridisation probes in chromosome and gene
 CC mapping, or in generating antisense RNA and DNA. They are also useful in
 CC preparing PRO polypeptides, in assays to identify other proteins or
 CC molecules involved in binding reaction, to generate transgenic animals or
 CC knockout animals, which in turn are useful in the development and
 CC screening of therapeutically useful reagents, for chromosome
 CC identification, and tissue typing. The PRO polypeptides and nucleic acid
 CC molecules are also useful in gene therapy, and as molecular weight
 CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
 CC used in diagnostic assays for PRO polypeptides, or for the affinity
 CC purification of the polypeptides from recombinant cell culture or natural
 CC sources. ABU69103-ABU69125 represent the human PRO polypeptides of the
 CC invention
 XX
 XX Sequence 136 AA;
 SQ

Query Match 99.9%; Score 724; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.2e-70;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGLPVLILLAGAPAPRPTPTCYSRMRALSQETEDFNLLQVSESEPCVRLPR 60
 Db 1 MRPGLPVLILLAGAPAPRPTPTCYSRMRALSQETEDFNLLQVSESEPCVRLPR 60
 QY 61 LYLDIENYCVLDKLRDFVASPPCKVQVDSLKDKARKLYTINNSFCRRDLVFLDDCNA 120
 Db 61 LYLDIENYCVLDKLRDFVASPPCKVQVDSLKDKARKLYTINNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPTVTLPRQR 136
 Db 121 LEYPIPTVTLPRQR 136

RESULT 7
 ABO19435
 ID ABO19435 standard; protein; 136 AA.
 XX ABO19435;
 XX 27-AUG-2003 (first entry)
 DT Human secreted / transmembrane polypeptide PRO4425.
 DE Human; gene therapy; diabetes; obesity; hypoinsulinaemia.
 KW Homo sapiens.
 OS
 XX US2003027249-A1.
 XX 06-FEB-2003.
 XX 16-AUG-2001; 2001US-00931836.
 XX 15-MAY-1998; 98US-0085579P.
 XX 15-DEC-1998; 98US-0112514P.
 XX 23-DEC-1998; 98US-0113300P.
 XX 23-DEC-1998; 98US-0113430P.
 XX 23-DEC-1998; 98US-0113605P.
 XX 23-DEC-1998; 98US-0113621P.
 XX 23-DEC-1998; 98US-0114140P.

PA (GETH) GENENTECH INC.
 XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-341326/32.
 DR N-PSDB; ACA06115.
 XX
 XX New PRO polypeptides and nucleic acid molecules, useful for diagnosing or
 PT treating diabetes mellitus, cancers, septic shock, inflammatory bowel
 PT disease or asthma, or in gene therapy, chromosome identification or
 PT tissue typing.
 XX
 XX Claim 12; Fig 34; 196pp; English.
 PS
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful in diagnosing or treating non
 CC -insulin dependent diabetes mellitus, cancers, septic shock, rheumatoid
 CC arthritis, graft-versus-host disease, stroke, cardiac ischaemia,
 CC psoriasis, inflammatory bowel disease or asthma. The PRO polynucleotide
 CC sequences may be used as hybridisation probes in chromosome and gene
 CC mapping, or in generating antisense RNA and DNA. They are also useful in
 CC preparing PRO polypeptides, in assays to identify other proteins or
 CC molecules involved in binding reaction, to generate transgenic animals or
 CC knockout animals, which in turn are useful in the development and
 CC screening of therapeutically useful reagents, for chromosome
 CC identification, and tissue typing. The PRO polypeptides and nucleic acid
 CC molecules are also useful in gene therapy, and as molecular weight
 CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
 CC used in diagnostic assays for PRO polypeptides, or for the affinity
 CC purification of the polypeptides from recombinant cell culture or natural
 CC sources. ABU69080-ABU69102 represent the human PRO polypeptides of the
 CC invention
 XX
 SQ Sequence 136 AA;
 Query Match 99.9%; Score 724; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.2e-70;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRTGPELVLLLAGAPAAAPTPTCTCYSRMALSQETTRDFNLLQVSEPCVRYLPR 60
 Db 1 MRTGPELVLLLAGAPAAAPTPTCTCYSRMALSQETTRDFNLLQVSEPCVRYLPR 60
 QY 61 LYLDIHNYCVLDKLDKFVSPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 Db 61 LYLDIHNYCVLDKLDKFVSPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
 QY 121 LEYPIPTVTTLPPDRQR 136
 Db 121 LEYPIPTVTTLPPDRQR 136
 RESULT 11
 ABU81560
 ID ABU81560 standard; protein; 136 AA.
 AC ABU81560;
 XX
 XX 24-JUN-2003 (first entry)
 XX
 XX Human secreted polypeptide PRO4425.
 XX
 KW Human; inflammatory disease; organ failure; atherosclerosis; cancer;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW differentiation disorder; cell adhesion disorder; skin disorder;
 KW neural receptor disorder; diabetic complication; tissue typing.
 XX
 OS Homo sapiens.
 XX
 XX US2002192751-A1.

XX 19-DEC-2002.
 XX 26-DEC-2001; 2001US-00036041.
 XX
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-DEC-1998; 98US-0112514P.
 PR 22-DEC-1998; 98US-0113300P.
 PR 23-DEC-1998; 98US-0113430P.
 PR 23-DEC-1998; 98US-0113605P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 12-DEC-1998; 98US-0114140P.
 PR 12-JAN-1999; 99US-0115552P.
 PR 22-JAN-1999; 99US-0116843P.
 PR 23-MAR-1999; 99US-0125774P.
 PR 23-MAR-1999; 99US-0125778P.
 PR 24-MAR-1999; 99US-0125826P.
 PR 31-MAR-1999; 99US-0127035P.
 PR 05-APR-1999; 99US-012706P.
 PR 13-APR-1999; 99US-0129122P.
 PR 21-APR-1999; 99US-0130359P.
 PR 27-APR-1999; 99US-0131270P.
 PR 27-APR-1999; 99US-0131291P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 04-MAY-1999; 99US-0132379P.
 PR 04-MAY-1999; 99US-0132383P.
 PR 14-MAY-1999; 99US-0132383P.
 PR 25-MAY-1999; 99US-0132383P.
 PR 08-JUN-1999; 99US-0138166P.
 PR 20-JUL-1999; 99US-0144791P.
 PR 03-AUG-1999; 99US-0146970P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99US-028551.
 PR 22-DEC-1999; 99US-030720.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021566.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 16-AUG-2001; 2001US-00931836.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-341079/32.
 XX N-PSDB; ACA67738.
 XX
 XX New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
 PT cancer.
 XX
 XX Claim 12; Fig 34; 195pp; English.
 PS
 XX The invention relates to an isolated nucleic acid that encodes a PRO
 CC polypeptide. The nucleic acids and polypeptides are useful for treating
 CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
 CC infertility, birth defects, premature aging, acquired immunodeficiency
 CC syndrome (AIDS), cancer, differentiation disorders, cell adhesion
 CC disorders, neural receptor disorders, skin disorders or diabetic
 CC complications. The nucleic acids are useful as hybridisation probes, in
 CC chromosome and gene mapping and in generating antisense RNA or DNA. The


```
RESULT 13
ABU08232
ID ABU08232 standard; protein; 136 AA.
AC
AC ABU08232;
XX
XX 13-SEP-2003 (first entry)
DT
DE
DE Human Pro4425 protein.
XX
XX Human; Pro4425; bone; cartilage; bone disorder; osteopathic;
KW gene therapy; cartilage disorder; bone development; osteoporosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Signal_peptide
FT Modified-site 16..22
FT /note= "N myristoylation site"
FT Protein 20..196
FT /label= Mature_Pro4425_protein
FT Modified-site 60..69
FT /note= "Tyrosine kinase phosphorylation site"
XX
XX US2003044897-A1.
XX
XX 06-MAR-2003.
XX
XX 13-DEC-2001; 2001US-00020419.
XX
XX 04-MAY-1999; 99US-0132379P.
PR
PR 01-MAR-2000; 2000WO-US005601.
PR
PR 20-JUN-2001; 2001WO-US019692.
PR
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH ) GENENTECH INC.
XX
XX Goddard A, Wood WI, Ye W, Zhang Z;
PI
XX WPI; 2003-479740/45.
XX
XX N-PSDB; ABX15048.
DR
XX
XX New Pro4425 polypeptide, useful for alleviating/treating and diagnosing
PT bone and cartilage disorders e.g. osteoporosis, and increasing bone
PT growth.
XX
XX Claim 10; Fig 2; 58pp; English.
PS
XX
XX This invention relates to a novel isolated PRO4425 polypeptide and the
CC nucleic acid sequence encoding it, this protein is expressed in early
CC bone and in cartilage and may be used to treat and diagnose bone
CC disorders. The invention also discloses an antibody that specifically
CC binds to the polypeptide and a method for alleviating bone disorders in a
CC mammal by administering a PRO4425 polypeptide or its agonist. The Pro4425
CC protein if the invention may have osteopathic activities and may be used
CC in gene therapy or to develop PRO4425 Agonist. The polypeptides and
CC nucleic acids of the invention are useful for alleviating/treating and
CC diagnosing bone and cartilage disorders, and increasing bone growth in
CC developing or injured bones. They are particularly useful for treating
CC osteoporosis. The present sequence represents the human Pro4425 protein
CC of the invention
XX
XX Sequence 136 AA;
SQ
Query Match 99.9%; Score 724; DB 6; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2e-70;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRTGFLPVLLLLAGAPARTPTTCYSRMALSQEITRDENILQVSEPEPCVRYLPR 60
DB 1 MRTGFLPVLLLLAGAPARTPTTCYSRMALSQEITRDENILQVSEPEPCVRYLPR 60
QY 61 LYLDIHNYCVLDKLRDEVASPPCKVQAQVDSLKDKAEKLYTIMNSFCRRDLVFLDDCNA 120
DB 61 LYLDIHNYCVLDKLRDEVASPPCKVQAQVDSLKDKAEKLYTIMNSFCRRDLVFLDDCNA 120
QY 121 LEYPIPVTTVLPRQR 136
DB 121 LEYPIPVTTVLPRQR 136
RESULT 14
ABO25143
ID ABO25143 standard; protein; 136 AA.
XX
XX ABO25143;
AC
AC 05-SEP-2003 (first entry)
DT
DE
DE Human secreted/transmembrane protein PRO4425.
XX
XX Human; PRO; secreted protein; transmembrane protein; septic shock;
KW gene therapy.
XX
XX Homo sapiens.
OS
XX
XX US2003044842-A1.
XX
XX 06-MAR-2003.
XX
XX 26-DEC-2001; 2001US-00036160.
XX
XX 15-MAY-1998; 98US-0085579P.
PR
PR 15-DEC-1998; 98US-0112514P.
PR
PR 22-DEC-1998; 98US-0113300P.
PR
PR 23-DEC-1998; 98US-0113430P.
PR
PR 23-DEC-1998; 98US-0113605P.
PR
PR 23-DEC-1998; 98US-0113621P.
PR
PR 12-JAN-1999; 98US-0114140P.
PR
PR 22-JAN-1999; 98US-0115552P.
PR
PR 23-MAR-1999; 99US-0125774P.
PR
PR 24-MAR-1999; 99US-0125826P.
PR
PR 31-MAR-1999; 99US-0127035P.
PR
PR 05-APR-1999; 99US-012706P.
PR
PR 13-APR-1999; 99US-0129122P.
PR
PR 21-APR-1999; 99US-0130359P.
PR
PR 27-APR-1999; 99US-0131270P.
PR
PR 27-APR-1999; 99US-0131272P.
PR
PR 04-MAY-1999; 99US-0131291P.
PR
PR 04-MAY-1999; 99US-0132379P.
PR
PR 04-MAY-1999; 99US-0132383P.
PR
PR 14-MAY-1999; 99WO-US010733.
PR
PR 25-MAY-1999; 99US-0135750P.
PR
PR 08-JUN-1999; 99US-0138166P.
PR
PR 20-JUL-1999; 99US-0144791P.
PR
PR 03-AUG-1999; 99US-0146970P.
PR
PR 29-OCT-1999; 99US-0162506P.
PR
PR 02-DEC-1999; 99WO-US028551.
PR
PR 22-DEC-1999; 99WO-US030720.
PR
PR 01-MAR-2000; 2000WO-US005601.
PR
PR 02-MAR-2000; 2000WO-US005841.
PR
PR 22-MAY-2000; 2000WO-US014042.
PR
PR 02-JUN-2000; 2000WO-US015264.
PR
PR 23-AUG-2000; 2000WO-US023522.
PR
PR 24-AUG-2000; 2000WO-US023328.
PR
PR 01-DEC-2000; 2000WO-US032678.
PR
PR 20-DEC-2000; 2000WO-US034956.
PR
PR 28-FEB-2001; 2001WO-US006520.
PR
PR 01-JUN-2001; 2001WO-US017800.
PR
PR 20-JUN-2001; 2001WO-US019692.
PR
PR 29-JUN-2001; 2001WO-US021066.
PR
PR 09-JUL-2001; 2001WO-US021735.
```

PR 16-AUG-2001; 2001US-00931836.
 XX (GETH) GENENTECH INC.
 PA Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-492260/46.
 DR N-PSDB; ACD42300.
 XX
 PT Novel secreted and transmembrane polypeptide for identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX
 PS Claim 12; Fig 34; 195pp; English.
 XX
 CC The invention relates to an isolated, secreted and transmembrane
 CC polypeptide, termed PRO polypeptide, PRO having at least 80 % sequence
 CC identity to any one of the 23 100-900 residue amino acid sequences, given
 CC in the specification or to a sequence encoded by a nucleic acid molecule
 CC deposited under any one of the ATCC accession numbers given in the
 CC specification. Also included are an isolated nucleic acid molecule having
 CC at least 80 % sequence identity to any one of 23 400-3500 nucleotide
 CC sequences given in the specification, (or a nucleotide sequence encoding
 CC PRO, a full-length PRO coding sequence, a full-length coding sequence of
 CC DNA deposited under any ATCC accession number given in the specification)
 CC or at least 80 % identity to a nucleotide sequence encoding PRO, lacking
 CC its associated signal peptide, a sequence encoding extracellular domain
 CC of PRO with or without its associated signal peptide, a vector comprising
 CC the PRO nucleic acid, a host cell comprising the vector, preparation of
 CC PRO, a chimeric molecule comprising PRO fused to a heterologous amino
 CC acid sequence and an anti-PRO antibody. PRO is useful for identifying
 CC anti/agonists or antagonists of PRO, preparing a variant of PRO, as
 CC molecular weight markers and PRO nucleic acid is useful for recombinantly
 CC expressing those markers. PRO is also useful as therapeutic agent. PRO is
 CC useful in assays to identify molecules or proteins which bind to PRO and
 CC for identifying inhibitors of PRO. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in generation of
 CC antisense RNA and DNA, for generating transgenic animals or knockout
 CC animals which in turn are useful in the development and screening of
 CC therapeutically useful reagents. PRO nucleic acid is also useful in
 CC mapping the gene which encodes the PRO and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome marker, and for generating probes for PCR,
 CC Northern analysis, Southern analysis and Western analysis. The antibody
 CC useful in diagnostic assays for PRO, for affinity purification of PRO,
 CC and for treating septic shock. PRO or the antibody is useful for the
 CC preparation of medicament for treating conditions which is responsive to
 CC the PRO polypeptide or anti-PRO antibody. PRO and PRO nucleic acid are
 CC useful for tissue typing. The present sequence represents a PRO protein
 XX
 SQ Sequence 136 AA;

Query Match 99.9%; Score 724; DB 7; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.2e-70;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTGGLPVLILLAGAPAAAPPTPTCYSMRALSQEITRDFNLLQVSEFPCVRYLR 60
 DB 1 MRTGGLPVLILLAGAPAAAPPTPTCYSMRALSQEITRDFNLLQVSEFPCVRYLR 60
 QY 61 LVLDIHNYCVLQKRFVAPSPCKVQVDSLQKARKLYTINNSCRDLVFLDDCNA 120
 DB 61 LVLDIHNYCVLQKRFVAPSPCKVQVDSLQKARKLYTINNSCRDLVFLDDCNA 120
 QY 121 LEYPIPTVTLVLPDRQR 136
 DB 121 LEYPIPTVTLVLPDRQR 136

RESULT 15
 ID AAE39113
 XX AAE39113 standard; protein; 136 AA.

AC AAE39113;
 XX 18-DEC-2003 (first entry)
 DE Human PRO4425 protein.
 XX Human; PRO protein; inflammation; nephropathy; bone disorder; arthritis;
 KW cartilage disorder; diabetes; gene therapy; antisense therapy.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Modified-site /label= Signal_peptide
 FT 16..22 /note= "N-myristoylation site"
 FT Protein 20..136
 FT /note= "Mature human PRO protein"
 FT Binding-site 60..69
 FT /note= "Tyrosine kinase phosphorylation site"
 XX US2003049733-A1.
 XX 13-MAR-2003.
 XX 26-DEC-2001; 2001US-00035958.
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-DEC-1998; 98US-0112514P.
 PR 23-DEC-1998; 98US-0113300P.
 PR 23-DEC-1998; 98US-0113430P.
 PR 23-DEC-1998; 98US-0113605P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 23-DEC-1998; 98US-0114140P.
 PR 12-JAN-1999; 99US-0115552P.
 PR 22-JAN-1999; 99US-0116843P.
 PR 23-MAR-1999; 99US-0125774P.
 PR 23-MAR-1999; 99US-0125778P.
 PR 31-MAR-1999; 99US-0127035P.
 PR 05-APR-1999; 99US-0127706P.
 PR 13-APR-1999; 99US-0129122P.
 PR 21-APR-1999; 99US-0130359P.
 PR 27-APR-1999; 99US-0131270P.
 PR 27-APR-1999; 99US-0131272P.
 PR 04-MAY-1999; 99US-0131291P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 04-MAY-1999; 99US-0132379P.
 PR 14-MAY-1999; 99US-0132383P.
 PR 14-MAY-1999; 99US-0132383P.
 PR 14-MAY-1999; 99US-0132383P.
 PR 08-JUN-1999; 99US-0138166P.
 PR 20-JUL-1999; 99US-0144791P.
 PR 03-AUG-1999; 99US-0146970P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99US-0162506P.
 PR 22-DEC-1999; 99US-0162506P.
 PR 01-MAR-2000; 2000US-0005601.
 PR 02-MAR-2000; 2000US-0005601.
 PR 22-MAY-2000; 2000US-0014042.
 PR 02-JUN-2000; 2000US-0015264.
 PR 23-AUG-2000; 2000US-0023522.
 PR 24-AUG-2000; 2000US-0023522.
 PR 01-DEC-2000; 2000US-0032678.
 PR 20-DEC-2000; 2000US-0034956.
 PR 28-FEB-2001; 2001US-0006520.
 PR 01-JUN-2001; 2001US-0017800.
 PR 20-JUN-2001; 2001US-0019692.
 PR 29-JUN-2001; 2001US-0021066.
 PR 09-JUL-2001; 2001US-0021735.
 PR 16-AUG-2001; 2001US-00931836.
 XX
 PA (GETH) GENENTECH INC.

XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-585109/55.
DR N-PSDB; AAD59366.
XX
PT New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT acids, useful for diagnosing, preventing and/or treating inflammation,
PT nephropathies, bone and cartilage disorders, and diabetes.
XX
PS Claim 12; Fig 34; 203pp; English.
XX
XX The invention relates to an isolated nucleic acid that encodes a PRO
CC polypeptide. The methods and compositions of the present invention are
CC useful for the diagnosis, prevention and/or treatment of inflammation,
CC nephropathies, bone and cartilage disorders, such as arthritis and
CC disorders that affect glucose or free fatty acid (FFA) uptake, such as
CC diabetes, hypoinulinaemia or hyperinsulinaemia. The PRO polypeptides are
CC also useful as molecular weight markers or for chromosome identification.
CC The PRO genes are useful as hybridisation probes or for screening
CC libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be
CC used in gene therapy and antisense therapy. The present sequence is human
CC PRO protein
XX
SQ Sequence 136 AA;
Query Match 99.9%; Score 724; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2e-70;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRTGPIPLVLLLLAGAPAAAPTPTTCYSRMALSQEITRDFNLLQVSEPCVRYLPR 60
Db 1 MRTGPIPLVLLLLAGAPAAAPTPTTCYSRMALSQEITRDFNLLQVSEPCVRYLPR 60
Qy 61 LYLDIHNVCVLDKLRDFVAPPCWKVAQVDSLKDKARKLYTIMNSFCERDLVFLDDCNA 120
Db 61 LYLDIHNVCVLDKLRDFVAPPCWKVAQVDSLKDKARKLYTIMNSFCERDLVFLDDCNA 120
Qy 121 LEYPIPTVTVLPDRQR 136
Db 121 LEYPIPTVTVLPDRQR 136

Search completed: February 25, 2004, 05:02:19
Job time : 61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:06:17 ; Search time 18 Seconds
(without alignments)
396.312 Million cell updates/sec

Title: US-10-023-282-310

Perfect score: 137

Sequence: 1 MTPGGLPVLLLLLAGAPAA.....CNALFYPIPTVTLPDRQX 137

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	99.3	136	C17_HUMAN	Q9nrri homo sapien
2	8	5.8	114	1 YPUD_BACSU	P17616 bacillus su
3	8	5.8	351	1 NOV_CHICK	P28686 gallus gall
4	8	5.8	353	1 NOV_COTJA	P42642 coturnix co
5	8	5.8	359	1 ASAL_HUMAN	Q02083 homo sapien
6	8	5.8	361	1 HALA_RABIT	P01894 oryctolagus
7	8	5.8	361	1 HALB_RABIT	P06340 oryctolagus
8	8	5.8	451	1 YOE2_STRAT	Q53884 streptomyce
9	8	5.8	519	1 PPBT_CHICK	Q92058 gallus gall
10	8	5.8	525	1 PDA2_HUMAN	Q13087 homo sapien
11	8	5.8	537	1 LG14_HUMAN	Q8n135 homo sapien
12	8	5.8	580	1 MM14_PIG	Q9xt90 sus scrofa
13	8	5.8	582	1 MM14_HUMAN	P50281 homo sapien
14	8	5.8	582	1 MM14_MOUSE	P53690 mus musculu
15	8	5.8	582	1 MM14_RABIT	Q95220 oryctolagus
16	8	5.8	582	1 MM14_RAT	Q10739 rattus norv
17	8	5.8	604	1 YFIC_BACSU	P54719 bacillus su
18	8	5.8	4563	1 APB_HUMAN	P04114 homo sapien
19	7	5.1	100	1 MIP2_MOUSE	P10889 mus musculu
20	7	5.1	100	1 MIP2_RAT	P10348 rattus norv
21	7	5.1	143	1 IL3_MACMU	P25140 macaca mula
22	7	5.1	152	1 IL3_HUMAN	P08700 homo sapien
23	7	5.1	152	1 IL3_HYLLA	P06740 hylabates l
24	7	5.1	152	1 IL3_PANTR	Q28809 pan troglod
25	7	5.1	160	1 GLUT_PETMA	Q9puri petromyzon
26	7	5.1	203	1 CLPI_MYXXA	O30612 myxococcus
27	7	5.1	205	1 ENGB_HAEIN	P46453 haemophilus
28	7	5.1	205	1 ENGB_PASMU	P57947 pasteurella
29	7	5.1	219	1 YGHB_SALTU	P18951 salmonella
30	7	5.1	220	1 PSD9_YEAST	P40555 saccharomyc
31	7	5.1	260	1 XBPI_HUMAN	P17861 homo sapien
32	7	5.1	283	1 YORS_ADEG1	P20747 avian adeno
33	7	5.1	285	1 AROE_CAUCR	Q9ac57 caulobacter

RESULT 1

ID	C17_HUMAN	STANDARD	PRT	136 AA
AC	Q9NRRI			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Cytokine-like protein C17 precursor.			
GN	C4ORF4			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.			
RC	TISSUE=Blood;			
RX	MEDLINE=20313895; PubMed=10857752;			
RA	Liu X., Rapp N., Deans R., Cheng L.;			
RT	"Molecular cloning and chromosomal mapping of a candidate cytokine			
RT	gene selectively expressed in human CD34+ cells.";			
RL	Genomics 65:283-292(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon;			
RX	MEDLINE=22398257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zensberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Specifically expressed in CD34+ hematopoietic			
CC	cells.			

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CC EMBL; AF193766; AAF73372.1; -;
 DR EMBL; BC031391; AAH31391.1; -;
 DR MIM; 607930; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005102; F:receptor binding; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 KW Signal.
 FT SIGNAL .1 19 POTENTIAL.
 FT CHAIN 20 136 CYTOKINE-LIKE PROTEIN C17.
 SQ SEQUENCE 136 AA; 15577 MW; 1CAEE1BFC31A3AE3 CRC64;
 Query Match 99.3%; Score 136; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.5e-121;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC 1 MRTGPLPVLLLLAGAPAAAPPTPTCYSRMRALSOEITRDFNLLQVSEPEPCVRYLPR 60
 Db 1 MRTGPLPVLLLLAGAPAAAPPTPTCYSRMRALSOEITRDFNLLQVSEPEPCVRYLPR 60
 Qy 61 LYLDHNYCVLDKURDFVAPSPCKVAQVDSLKQKARKLYTIMNSFCRRDLVFLDDCNA 120
 Db 61 LYLDHNYCVLDKURDFVAPSPCKVAQVDSLKQKARKLYTIMNSFCRRDLVFLDDCNA 120
 Qy 121 LEYPIPVTTVLPDRQR 136
 Db 121 LEYPIPVTTVLPDRQR 136
 RESULT 2
 YPUD BACSU STANDARD; PRT; 114 AA.
 ID YPUD BACSU STANDARD; PRT; 114 AA.
 AC P17616;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein ypuD (ORF4).
 GN YPUD OR BSU23300.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / Marburg;
 RX MEDLINE=95020538; PubMed=7934829;
 RA Sorokin A.V., Zumbstein E., Azevedo V., Ehrlich S.D., Serror P.;
 RT "The organization of the Bacillus subtilis 168 chromosome region
 between the spoVA and serA genetic loci, based on sequence data.";
 RL Mol. Microbiol. 10:385-395(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / SHGW;
 RA Mironov V.N.;
 RN Thesis (1989), USSR Academy of Sciences, Russia.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=3384377;
 RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Glim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Guiseppe H., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nohack M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Takakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Toseki V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 RT Nature 390:249-256(1997).
 CC -----
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 CC -----
 CC EMBL; L09228; AAA67479.1; -;
 DR EMBL; X51510; CAA35877.1; -;
 DR EMBL; Z99116; CAB14262.1; -;
 DR PIR; S45541; S45541.
 DR Subtilist; BG10516; YpuD.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 114 AA; 12754 MW; 393036DF1A2DFC6D CRC64;
 Query Match 5.8%; Score 8; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 VLLLLLAG 16
 Db 13 VLLLLLAG 20
 RESULT 3
 NOV CHICK
 ID NOV CHICK STANDARD; PRT; 351 AA.
 AC P28686;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NOV protein precursor (Nephroblastoma overexpressed gene protein).
 GN NOV OR CCN3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown leghorn;
 RX MEDLINE=92107157; PubMed=1309586;
 RA Joliet V., Martinezie C., Dambrine G., Plassiat G., Brisac M.,
 RA Crochet J., Perbal B.;
 RT "Proviral rearrangements and overexpression of a new cellular gene
 RT (nov) in myeloblastosis-associated virus type 1-induced
 RT nephroblastomas.";
 RL Mol. Cell. Biol. 12:10-21(1992).
 CC -i- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
 CC GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WITH
 CC TUMORIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED VERSION
 CC OF NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEF) IS SUFFICIENT
 CC TO INDUCE THE TRANSFORMATION OF CEF IN VITRO.
 CC -i- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN
 CC MUSCLE AND INTESTINE, IN THE EMBRYO, LUNG AND LESS SO IN BRAIN AND
 CC SPLEEN, IN ADULT CHICKEN.
 CC -1- DEVELOPMENTAL STAGE: NAVI-INDUCED NEPHROBLASTOMAS EXPRESS A HIGH
 CC LEVEL OF NOV GENE WHOSE TRANSCRIPTION IS NORMALLY ARRESTED IN
 CC ADULT KIDNEY.
 CC -1- SIMILARITY: Belongs to the CCN family.
 CC -1- SIMILARITY: Contains 1 IGFBP domain.
 CC -1- SIMILARITY: Contains 1 WFPC domain.
 CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
 CC -1- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X59284; CAA41975.1; --
 CC PIR: S20078; S20078.
 CC InterPro: IPR006208; Cys_knot.
 CC InterPro: IPR006207; Cys_knot_C.
 CC InterPro: IPR000867; Insl_gro_fac_pr.
 CC InterPro: IPR000884; TSPL.
 CC InterPro: IPR001007; WVF_C.
 CC Pfam: PF00007; Cys_knot; 1.
 CC Pfam: PF00219; IGFBP; 1.
 CC Pfam: PF00090; tsp_1; 1.
 CC Pfam: PF00093; wvc; 1.
 CC SMART: SM00041; CT; 1.
 CC SMART: SM00121; IB; 1.
 CC SMART: SM00209; TSPL; 1.
 CC SMART: SM00214; VMC; 1.
 CC PROSITE: PS01185; CTCK_1; 1.
 CC PROSITE: PS01225; CTCK_2; 1.
 CC PROSITE: PS00222; IGF_BINDING; 1.
 CC PROSITE: PS50092; TSPL; 1.
 CC PROSITE: PS01208; WVEC_1; 1.
 CC PROSITE: PS50184; WVEC_2; 1.
 CC Proto-oncogene; Growth factor; Signal.
 CC SIGNAL 1 24 POTENTIAL.
 CC CHAIN 25 351 NOV PROTEIN.
 CC DOMAIN 31 103 IGFBP.
 CC DOMAIN 104 170 WFPC.
 CC DOMAIN 201 246 TSP TYPE-1.
 CC DOMAIN 258 332 CTCK.
 CC DISULFID 258 295 BY SIMILARITY.
 CC DISULFID 275 309 BY SIMILARITY.
 CC DISULFID 286 325 BY SIMILARITY.
 CC DISULFID 289 327 BY SIMILARITY.
 CC DISULFID 294 331 BY SIMILARITY.
 CC CARBOHYD 274 274 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 351 AA; 38268 MW; 1ECB3FA3058C6797 CRC64;

Query Match 5.8%; Score 8; DB 1; Length 351;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
 |||||
 Db 9 LPVLLLLL 16

RESULT 4

NOV_COTJA STANDARD; PRT; 353 AA.
 AC P42642;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NOV protein precursor (Nephroblastoma overexpressed gene protein).

GN NOV OR CCN3.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Coturnix.
 OC NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Weiskirchen R., Bister K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Immediate-early protein likely to play a role in cell
 CC growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Belongs to the CCN family.
 CC -1- SIMILARITY: Contains 1 IGFBP domain.
 CC -1- SIMILARITY: Contains 1 WFPC domain.
 CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
 CC -1- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U13063; AAA21128.1; --
 CC InterPro: IPR006208; Cys_knot.
 CC InterPro: IPR006207; Cys_knot_C.
 CC InterPro: IPR000867; Insl_gro_fac_pr.
 CC InterPro: IPR000884; TSPL.
 CC InterPro: IPR001007; WVF_C.
 CC Pfam: PF00007; Cys_knot; 1.
 CC Pfam: PF00219; IGFBP; 1.
 CC Pfam: PF00090; tsp_1; 1.
 CC Pfam: PF00093; wvc; 1.
 CC SMART: SM00041; CT; 1.
 CC SMART: SM00121; IB; 1.
 CC SMART: SM00209; TSPL; 1.
 CC SMART: SM00214; VMC; 1.
 CC PROSITE: PS01185; CTCK_1; 1.
 CC PROSITE: PS01225; CTCK_2; 1.
 CC PROSITE: PS00222; IGF_BINDING; 1.
 CC PROSITE: PS50092; TSPL; 1.
 CC PROSITE: PS01208; WVEC_1; 1.
 CC PROSITE: PS50184; WVEC_2; 1.
 CC Proto-oncogene; Growth factor; Signal.
 CC SIGNAL 1 26 POTENTIAL.
 CC CHAIN 27 353 NOV PROTEIN.
 CC DOMAIN 33 105 IGFBP.
 CC DOMAIN 106 172 WFPC.
 CC DOMAIN 203 248 TSP TYPE-1.
 CC DOMAIN 260 334 CTCK.
 CC DISULFID 260 297 BY SIMILARITY.
 CC DISULFID 277 311 BY SIMILARITY.
 CC DISULFID 288 327 BY SIMILARITY.
 CC DISULFID 291 329 BY SIMILARITY.
 CC DISULFID 296 333 BY SIMILARITY.
 CC CARBOHYD 276 276 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 353 AA; 38667 MW; 717D9F8533882E89 CRC64;

Query Match 5.8%; Score 8; DB 1; Length 353;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
 |||||
 Db 9 LPVLLLLL 16

RESULT 5
 ASAL_HUMAN

```
ID ASAL HUMAN STANDARD; PRT; 359 AA.
AC Q02083; Q96EV2; Q9BRA8;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE "N-acylsphingosine amido-hydrolyase-like precursor (EC 3.5.1.-) (Acid
DE ceramidase-like protein) (ASAH-like protein)."
GN ASAH OR PLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND SUBCELLULAR
RP LOCATION.
RC TISSUE=Placenta;
RX MEDLINE=20079156; PubMed=10610717;
RA Hong S.-B., Li C.-M., Rhee H.-J., Park J.-H., He X., Levy B.,
RA Yoo O.-J., Schuchman E.H.;
RT "Molecular cloning and characterization of a human cDNA and gene
RT encoding a novel acid ceramidase-like protein."
RL Genomics 62:232-241(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Stausberg R.L., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavini T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT human and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 81-359 FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=93077043; PubMed=1446826;
RA Goodchild N.L., Wilkinson D.A., Mager D.L.;
RT "A human endogenous long terminal repeat provides a polyadenylation
RT signal to a novel, alternatively spliced transcript in normal
RT placenta."
RL Gene 121:287-294(1992).
CC -!- SUBCELLULAR LOCATION: Lysosomal (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=Q02083-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q02083-2; Sequence=VSP_000330;
CC Note=Incomplete sequence;
CC Name=3;
CC IsoId=Q02083-3; Sequence=VSP_000328, VSP_000329;
CC -!- TISSUE SPECIFICITY: Expressed in numerous tissues, with highest
CC levels in liver and kidney, followed by pancreas.
CC -!- SIMILARITY: Belongs to the acid ceramidase family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; BC006388; AA06388.1; ALT_INIT.
DR EMBL; BC011854; AA011854.1; -.
DR EMBL; M92449; AAA60119.1; -.
DR MIM; 607459; -.
DR HGNC; 736; ASAH.
DR InterPro; IPR003199; Chlgly_hydrolase.
DR Pfam; PF02275; CBAH; 1.
KW Hydrolase; Signal; Alternative splicing.
FT SIGNAL 1 28
FT CHAIN 29 359 N-ACYLSPHINGOSINE AMIDOHYDROLASE-LIKE.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 198 199 KG -> PE (in isoform 3).
FT VARSPLIC 200 359 /FTid=VSP_000328.
FT VARSPLIC 324 359 Missing (in isoform 3).
FT VARSPLIC 324 359 /FTid=VSP_000329.
FT CONFLICT 147 147 P -> A (IN REF. 3).
FT CONFLICT 240 240 T -> S (IN REF. 3).
FT CONFLICT 250 250 V -> L (IN REF. 3).
SQ SEQUENCE 359 AA; 40032 MW; A8E8B471383B872A CRC64;
Query Match 5.8%; Score 8; DB 1; Length 359;
Best Local Similarity 100.0%; Pred.No.5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 LLLLLL 17
Db 16 LLLLLL 23
RESULT 6
HAIA RABIT
ID HAIA RABIT STANDARD; PRT; 361 AA.
AC P01894;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RLA class I histocompatibility antigen, alpha chain 11/11 precursor.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84290724; PubMed=6432910;
RA Tykocinski M.L., Marche P.N., Max E.E., Kindt T.J.;
RT "Rabbit class I MHC genes: cDNA clones define full-length transcripts
RT of an expressed gene and a putative pseudogene."
RL J. Immunol. 133:2261-2269(1984).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -----
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DR EMBL: K02441; AAA98729.1; --
DR PIR: A02193; HLRB.
DR HSSP: Q30201; IA6Z.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR PRINTS: PR01638; MHC_I.
DR ProDom: PD000050; MHC_I; 1.
DR SMART: SM00407; IGCL_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
DR MHC I; Transmembrane; Glycoprotein; Signal.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 361
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 329
FT CARBOHYD 330 361
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 361 AA; 40447 MW; 580B673323CIAE35 CRC64;

Query Match 5.8%; Score 8; DB 1; Length 361;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLLAGA 17
DB 9 LLLLLLAGA 16

RESULT 7
HAIR_RABIT STANDARD; PRT; 361 AA.
AC P06140;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RLA class I histocompatibility antigen, alpha chain 19-1 precursor.
OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85103547; PubMed=3917974;
RA Marche P.N., Tykocinski M.L., Max E.E., Kindt T.J.;
RT "Structure of a functional rabbit class I MHC gene: similarity to
human class I genes."
RL Immunogenetics 21:71-82(1985).
CC -1- FUNCTION: Involved in the presentation of foreign antigens to the
immune system.
CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
CC
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CC
CC EMBL: K02819; AAA98730.1; --
DR PIR: I46858; IA6Z.
DR HSSP: Q30201; IA6Z.

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR PRINTS: PR01638; MHC_I.
DR ProDom: PD000050; MHC_I; 1.
DR SMART: SM00407; IGCL_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
DR MHC I; Transmembrane; Glycoprotein; Signal.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 361
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 329
FT CARBOHYD 330 361
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 361 AA; 40455 MW; C06FDB88B7ED0546 CRC64;

Query Match 5.8%; Score 8; DB 1; Length 361;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLLAGA 17
DB 9 LLLLLLAGA 16

RESULT 8
YOE2_STRAT STANDARD; PRT; 451 AA.
AC Q53684;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 48.5 kDa protein in oled 5' region precursor (ORF2).
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1890;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 11891;
RX MEDLINE=94063510; PubMed=8244027;
RA Hernandez C., Olano C., Mendez C., Salas J.A.;
RT "Characterization of a Streptomyces antibioticus gene cluster
encoding a glycosyltransferase involved in oleandomycin
inactivation."
RL Gene 134:139-140(1993).
CC -1- FUNCTION: MAY PARTICIPATE IN OLEANDOMYCIN GLYCOSYLATION AND
SECRETION DURING ANTIBIOTIC PRODUCTION.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Potential).
CC
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CC
CC EMBL: Z22577; CAA80300.1; --
DR PIR: S78104; S78104.
DR InterPro: IPR000437; Prok_lipoprot_S.
DR InterPro: IPR006059; SBP_bac_1.

```

DR Pfam; PF01547; SBP_bac_1; 1.
 DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
 KW Hypothetical protein; Membrane; Lipoprotein; Signal; Palmitate.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 451 HYPOTHETICAL 48.5 kDa PROTEIN IN OILED
 5 REGION.
 FT LIPID 19 19 N-palmitoyl cysteine (Potential).
 FT LIPID 19 19 S-diacylglycerol cysteine (Potential).
 SQ SEQUENCE 451 AA; 48542 MW; B8B2DF4AB80CC5F2 CRC64;
 Query Match 5.8%; Score 8; DB 1; Length 451;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 VLLLLLAG 16
 DB 11 VLLLLLAG 18
 RESULT 9
 PPBT CHICK STANDARD; PRT; 519 AA.
 AC Q92058;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alkaline phosphatase, tissue-nonspecific isozyme precursor
 (EC 3.1.3.1) (AP-TNAP) (Liver/bone/kidney isozyme).
 GN ALPL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96107571; PubMed=8553025;
 RA Crawford K., Weissig H., Binette F., Millan J.L., Goetinck P.F.;
 RT "Tissue-nonspecific alkaline phosphatase participates in the
 RT establishment and growth of feather germs in embryonic chick skin
 RT cultures";
 RL Dev. Dyn. 204:48-56(1995).
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the alkaline phosphatase family.
 CC
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 CC
 DR EMBL; U19108; AAA92562.1; -
 DR HSP; P00634; 2ANH.
 DR InterPro; IPR001952; Alk phosphatase.
 DR Pfam; PF00245; alk phosphatase; 1.
 DR PRINTS; PR00113; ALKPHPTASE.
 DR PRODOM; PD001868; Alk.phosphatase; 1.
 DR SMART; SM000098; alkppc; 1.
 DR PROSITE; PS00123; ALKALINE PHOSPHATASE; 1.
 KW Hydroxylase; Zinc; Magnesium; Phosphorylation; Transmembrane;
 KW Multigene family; Glycoprotein; GPI-anchor; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 519 ALKALINE PHOSPHATASE, TISSUE-NONSPECIFIC
 ISOZYME.
 FT ACT_SITE 109 109 PHOSPHOSERINE INTERMEDIATE
 (BY SIMILARITY).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 229 229 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 278 278 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 429 429 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 519 AA; 56760 MW; 7934C0EEC3B17B89 CRC64;
 Query Match 5.8%; Score 8; DB 1; Length 519;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LPVLLLLL 14
 DB 509 LPVLLLLL 516
 RESULT 10
 PDA2 HUMAN STANDARD; PRT; 525 AA.
 AC Q13087; Q96KJ6; Q9BW95;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein disulfide isomerase A2 precursor (EC 5.3.4.1) (PDIP).
 GN PDIP OR PDIA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 15-525 FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=96152236; PubMed=8561901;
 RA Desilva M.G., Lu J., Donadel G., Modi W.S., Xie H., Notkins A.L.,
 RA Lan M.S.;
 RT "Characterization and chromosomal localization of a new protein
 RT disulfide isomerase, PDIP, highly expressed in human pancreas";
 RL DNA Cell Biol. 15:9-16(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21096910; PubMed=11157797;
 RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT Mb of the short arm of human chromosome 16";
 RL Hum. Mol. Genet. 10:339-352(2001).
 RN [3]
 RP SEQUENCE OF 3-525 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=2338257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- CATALYTIC ACTIVITY: Rearrangement of both intrachain and
 CC interchain disulfide bonds in proteins to form the native
 CC structures.

CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in pancreas.
 CC -1- SIMILARITY: Contains 2 thioredoxin domains.
 CC -----
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 CC -----
 CC EMBL; U19948; AAC50401.1; -;
 CC EMBL; AE006463; AAK61223.1; -;
 CC EMBL; BC000537; AAH00537.1; -;
 CC HSP; P07237; IMEX.
 CC Genew; HGNC:14180; PDIP.
 CC MIM; 608012; -;
 CC GO; GO:0005783; C:endoplasmic reticulum; TAS.
 CC GO; GO:0003756; P:protein disulfide isomerase activity; TAS.
 CC GO; GO:0006457; P:protein folding; TAS.
 CC GO; GO:0006621; P:protein-ER retention; TAS.
 CC InterPro; IPR005788; Disulphid_ism.
 CC InterPro; IPR005792; Disulphid_ism.
 CC InterPro; IPR000886; ER target_S.
 CC InterPro; IPR006662; Thioered.
 CC InterPro; IPR006663; Thioredox_dom2.
 CC Pfam; PF00085; Thioered; 3.
 CC PRINTS; PR00421; THIOREDOXIN.
 CC TIGRFAMs; TIGR01130; ER_PDI_fam; 1.
 CC TIGRFAMs; TIGR01126; pdi_dom; 2.
 CC PROSITE; PS00194; THIOREDOXIN; 2.
 CC REDOXITE; PS00014; ER_TARGET; 1.
 CC Redox-active center; Isomerase; Endoplasmic reticulum; Repeat; Signal.
 CC -----
 CC FT SIGNAL 1 21 POTENTIAL.
 CC FT CHAIN 22 525 PROTEIN DISULFIDE ISOMERASE A2.
 CC FT DISULFID 71 74 REDOX-ACTIVE (BY SIMILARITY).
 CC FT DISULFID 418 421 REDOX-ACTIVE (BY SIMILARITY).
 CC FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 516 516 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SITE 522 525 PREVENT SECRETION FROM ER (POTENTIAL).
 CC FT CONFLICT 3 5 RQL -> ARG (IN REF. 2).
 CC FT CONFLICT 15 15 R -> M (IN REF. 1).
 CC FT CONFLICT 502 502 P -> S (IN REF. 1).
 CC FT CONFLICT 502 502 P -> S (IN REF. 1).
 CC SQ SEQUENCE 525 AA; 58206 MW; B741851AA2CA0540 CRC64;
 CC -----
 CC Query Match 5.8%; Score 8; DB 1; Length 525;
 CC Best Local Similarity 100.0%; Pred. No. 7;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Qy 7 LPVLLLL 14
 CC Db 6 LPVLLLL 13
 CC -----
 CC RESULT 11
 CC LGI4 HUMAN
 CC ID LGI4 HUMAN STANDARD; PRT; 537 AA.
 CC AC Q8N135;
 CC DT 10-OCT-2003 (Rel. 42, Created)
 CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Leucine-rich repeat LGI family member 4 precursor (Leucine-rich
 CC DE glioma-inactivated protein 4) (LGI-like protein 3).
 CC GN LGI4 OR LGI3.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=22017856; PubMed=12023020;

RA Gu W., Wevers A., Schroder H., Grzeschik K.H., Derst C., Brodtkorb E.,
 RA de Vos R., Steinlein O.K.;
 RA "The LGI1 gene involved in lateral temporal lobe epilepsy belongs to a
 RA RT new subfamily of leucine-rich repeat proteins.";
 RA FEBS Lett. 519:71-76(2002).
 RA [2]
 RA SEQUENCE FROM N.A.
 RA MEDLINE=22090568; PubMed=12095917;
 RA Scheel H., Tomiuk S., Hofmann K.;
 RA "A common protein interaction domain links two recently identified
 RA RT epilepsy genes.";
 RA Hum. Mol. Genet. 11:1757-1762(2002).
 RA [3]
 RA SEQUENCE FROM N.A.
 RA MEDLINE=22207944; PubMed=12217514;
 RA Staub E., Perez-Tur J., Siebert R., Moschonas N.K.,
 RA Deloukas P., Hinzmann B.;
 RA "The novel EPTP repeat defines a superfamily of proteins implicated in
 RA RT epileptic disorders.";
 RA Trends Biochem. Sci. 27:441-444(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- SIMILARITY: Contains 3 EAR repeats.
 CC -1- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
 CC -----
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 CC -----
 CC EMBL; AF467954; AAM49552.1; -;
 CC EMBL; AJ487959; CAD32306.1; -;
 CC EMBL; AJ487519; CAD31787.1; -;
 CC Genew; HGNC:18712; LGI4.
 CC InterPro; IPR009039; EAR.
 CC InterPro; IPR005492; EPTP.
 CC InterPro; IPR001611; LRR.
 CC InterPro; IPR000483; LRR_Cterm.
 CC InterPro; IPR003591; LRR_type.
 CC Pfam; PF03736; EPTP; 2.
 CC Pfam; PF00560; LRR; 3.
 CC Pfam; PF01463; LRRCT; 1.
 CC SMART; SM00082; LRRCT; 1.
 CC PROSITE; PS00912; EAR; 3.
 CC Repeat; Leucine-rich repeat; Signal.
 CC FT SIGNAL 1 19 POTENTIAL.
 CC FT CHAIN 20 537 LEUCINE-RICH REPEAT LGI FAMILY MEMBER 4.
 CC FT REPEAT 51 74 LRR 1.
 CC FT REPEAT 75 98 LRR 2.
 CC FT REPEAT 99 122 LRR 3.
 CC FT REPEAT 123 146 LRR 4.
 CC FT REPEAT 209 252 EAR 1.
 CC FT REPEAT 350 394 EAR 2.
 CC FT REPEAT 395 439 EAR 3.
 CC FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 537 AA; 59141 MW; 47B920C809679926 CRC64;
 CC -----
 CC Query Match 5.8%; Score 8; DB 1; Length 537;
 CC Best Local Similarity 100.0%; Pred. No. 7.2;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Qy 10 LLLLLLAGA 17
 CC Db 7 LLLLLLAGA 14
 CC -----
 CC RESULT 12
 CC MM14 FIG
 CC ID MM14 FIG STANDARD; PRT; 580 AA.
 CC AC Q9XT90;
 CC DT 16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Matrix metalloproteinase-14 precursor (BC 3.4.24.80) (MMP-14)
Membrane-type matrix metalloproteinase 1 (MT-MMP 1) (MTMMP1)
(Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MTMMP).
MMP14.
Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
MEDLINE=99095929; PubMed=9881602;
RA Caron C., Xue J., Bartlett J.D.;
RA "Expression and localization of membrane type 1 matrix
RT metalloproteinase in tooth tissues.";
RL Matrix Biol. 17:501-511(1998).
CC -!- FUNCTION: Seems to specifically activate progelatinase A. May thus
CC trigger invasion by tumor cells by activating progelatinase A on
CC the tumor cell surface (By similarity). May play a role in the
CC biomineralization of enamel and dentin.
CC -!- CATALYTIC ACTIVITY: Endopeptidase activity. Activates
CC progelatinase A by cleavage of the propeptide at 37-Asn-|-Leu-38.
CC Other bonds hydrolyzed include 35-Gly-|-Ile-36 in the propeptide
CC of collagenase 3, and 341-Asn-|-Phe-342, 441-Asp-|-Leu-442 and
CC 354-Gln-|-Thr-355 in the aggrecan interglobular domain.
CC -!- COFACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -!- TISSUE SPECIFICITY: Highly expressed in developing tooth tissues.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; AF067419; RAD38324.1; -.
HSP; P08254; 1HFS.
MEROPS; M10.014; -.
InterPro; IPR000585; Hemopexin.
InterPro; IPR001818; Pept_M10A_M12B.
InterPro; IPR006025; Pept_M_Zn_BS.
InterPro; IPR006026; Peptidase_M.
Pfam; PF00045; hemopexin; 4.
Pfam; PF00413; Peptidase_M10; 1.
Pfam; PF03933; Peptidase_M10_N; 1.
PRINTS; PR00138; MATRININ.
SMART; SM00120; HX; 4.
SMART; SM00235; ZnMc; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium; Signal;
Transmembrane.
FT SIGNAL 1 28 POTENTIAL.
FT PROPEP 29 109 ACTIVATION PEPTIDE.
FT CHAIN 110 580 MATRIX METALLOPROTEINASE-14.
FT DOMAIN 539 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 540 560 POTENTIAL.
FT DOMAIN 561 580 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 561 580 HEMOPEXIN-LIKE.
FT SITE 91 91 CYSTEINE SWITCH (POTENTIAL).
FT METAL 237 237 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 238 238 BY SIMILARITY.
FT METAL 241 241 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 247 247 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 317 506 BY SIMILARITY.
SQ SEQUENCE 580 AA; 65934 MW; B7B2C2C569A96CAC CRC64;

Query Match 5.8%; Score 8; DB 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
| | | | |
DB 542 LPVLLLLL 549

RESULT 13
MM14 HUMAN
ID MM14 HUMAN STANDARD; PRT; 582 AA.
AC P50281; O92678;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Matrix metalloproteinase-14 precursor (BC 3.4.24.80) (MMP-14)
DE Membrane-type matrix metalloproteinase 1 (MT-MMP 1) (MTMMP1)
DE Membrane-type-1 matrix metalloproteinase (MT1-MMP) (MTMMP) (MMP-
DE X1).
DE MM14.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94286011; PubMed=8015608;
RA Sato H., Takino T., Okada Y., Cao J., Shinagawa A., Yamamoto E.,
RA Seiki M.;
RA "A matrix metalloproteinase expressed on the surface of invasive
RT tumour cells.";
RT Nature 370:61-65(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95237627; PubMed=7721107;
RA Takino T., Sato H., Yamamoto E., Seiki M.;
RT "Cloning of a human gene potentially encoding a novel matrix
RT metalloproteinase having a C-terminal transmembrane domain.";
RT Gene 155:293-298(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95224014; PubMed=7708715;
RA Okada A., Bellocq J.P., Rouyer N., Chenard M.P., Rio M.C.,
RA Chambon P., Basset P.;
RT "Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in
RT stromal cells of human colon, breast, and head and neck carcinomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2730-2734(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95377289; PubMed=7649159;
RA Will H., Hinzmann B.;
RT "cDNA sequence and mRNA tissue distribution of a novel human matrix
RT metalloproteinase with a potential transmembrane segment.";
RL Eur. J. Biochem. 231:602-608(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Luo G.X., Reisfeld R.A., Strongin A.Y.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Lohi J.L., Westermarck J., Kaehaeri V.M., Keski-Oja J.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Seems to specifically activate progelatinase A. May thus
CC trigger invasion by tumor cells by activating progelatinase A on
CC the tumor cell surface.
CC -!- CATALYTIC ACTIVITY: Endopeptidase activity. Activates
CC progelatinase A by cleavage of the propeptide at 37-Asn-|-Leu-38.
CC Other bonds hydrolyzed include 35-Gly-|-Ile-36 in the propeptide
CC of collagenase 3, and 341-Asn-|-Phe-342, 441-Asp-|-Leu-442 and

354-Gln-|-Thr-355 in the aggrecan interglobular domain.
 -|- COFACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).
 -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 -|- TISSUE SPECIFICITY: In stromal cells of colon, breast, and head and neck.
 -|- SIMILARITY: Belongs to peptidase family M10A.
 -|- SIMILARITY: Contains 1 hemopexin-like domain.

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 EMBL; D26512; BAA05519.1; -;
 EMBL; X83535; CAA58519.1; -;
 EMBL; Z48481; CAA88372.1; -;
 EMBL; U41078; AAB83770.1; -;
 EMBL; X90925; CAA82432.1; -;
 PIR; I38028; I38028.
 PDB; 1BQQ; 23-AUG-01.
 PDB; 1BUV; 02-SEP-99.
 MEROPS; M10.014; -;
 Genew; HGNC:7160; MMP14.
 MIM; 600754; -;
 GO; GO:0005887; C: integral to plasma membrane; TAS.
 GO; GO:0004222; F: metalloendopeptidase activity; TAS.
 GO; GO:0008270; F: zinc ion binding; TAS.
 GO; GO:0006508; P: proteolysis and peptidolysis; TAS.
 InterPro; IPR000585; Hemopexin.
 InterPro; IPR001818; Pept_M10A_M12B.
 InterPro; IPR006025; Pept_M_Zn_BS.
 InterPro; IPR006026; Peptidase_M.
 Pfam; PF00045; hemopexin; 4.
 Pfam; PF00413; Peptidase_M10; 1.
 Pfam; PF03933; Peptidase_M10_N; 1.
 PRINTS; PR00138; MATRXIN.
 SMART; SMO0120; HX; 4.
 SMART; SMO0235; ZnMG; 1.
 PROSITE; PS00024; HEMOPEXIN; 1.
 PROSITE; PS00142; ZINC_PROPEASE; 1.
 PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium; Signal;
 Transmembrane; 3d-structure.
 SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 111 ACTIVATION PEPTIDE.
 FT CHAIN 112 582 MATRIX METALLOPROTEINASE-14.
 FT DOMAIN 112 541 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 542 562 POTENTIAL.
 FT DOMAIN 563 582 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 316 511 HEMOPEXIN-LIKE.
 FT SITE 93 93 CYSTEINE SWITCH (POTENTIAL).
 FT METAL 239 239 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT SITE 240 240 BY SIMILARITY.
 FT METAL 243 243 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 249 249 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 319 508 BY SIMILARITY.
 FT CONFLICT 338 338 K -> E (IN REF. 2, 4, 5 AND 6).
 FT CONFLICT 500 500 S -> P (IN REF. 6).
 SQ SEQUENCE 582 AA; 65883 MW; EFCEDCE6A41116F9 CRC64;

Query Match 5.8%; Score 8; DB 1; Length 582;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 7 LPVLLLL 14
 Db 544 LPVLLLL 551
 RESULT 14

MM14_MOUSE
 ID MM14_MOUSE STANDARD; PRT; 582 AA.
 AC P53690; O08645; O35369;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)
 DE (Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTMMP1)
 DE (Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MMP-X1) (MT-MMP).
 GN MMP14 OR MTMMP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=95224014; PubMed=7708715;
 RA Okada A., Bellocq J.P., Rouyer N., Chenard M.P., Rio M.C., Chambon P., Basset P.;
 RT "Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells of human colon, breast, and head and neck carcinomas."; Proc. Natl. Acad. Sci. U.S.A. 92:2730-2734 (1995).
 RL [2]
 RP REVISIONS.
 RA Odaka A.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=129/SV;
 RC MEDLINE=97467335; PubMed=9325265;
 RA Apte S.S., Fukai N., Beier D.R., Olsen B.R.;
 RT "The matrix metalloproteinase-14 (MMP-14) gene is structurally distinct from other MMP genes and is co-expressed with the TIMP-2 gene during mouse embryogenesis."; J. Biol. Chem. 272:25511-25517 (1997).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Kidney;
 RX MEDLINE=98311877; PubMed=9648071;
 RA Ota K., Stetler-Stevenson W.G., Yang Q., Kumar A., Wada J., Kashihara N., Wallner E.I., Kanwar Y.S.;
 RT "Cloning of murine membrane-type-1-matrix metalloproteinase (MT-1-MMP) and its metanephric developmental regulation with respect to MMP-2 and its inhibitor."; Kidney Int. 54:131-142 (1998).
 RL [5]
 RP FUNCTION.
 RX MEDLINE=99449306; PubMed=10520996;
 RA Holmbeck K., Bianco P., Caterina J., Yamada S., Kromer M., Kuznetsov S.A., Mankani M., Robey P.G., Poole A.R., Pidoux I., Ward J.M., Birkedal-Hansen H.;
 RT "MT1-MMP-deficient mice develop dwarfism, osteopenia, arthritis, and connective tissue disease due to inadequate collagen turnover."; Cell 99:81-92 (1999).
 RL -|- FUNCTION: Endopeptidase that degrades various components of the extracellular matrix, such as collagen. Activates progelatinase A. Essential for pericellular collagenolysis and modeling of skeletal and extracellular connective tissues during development.
 CC -|- CATALYTIC ACTIVITY: Endopeptidase activity. Activates progelatinase A by cleavage of the propeptide at 37-Asn-|-Leu-38. Other bonds hydrolyzed include 35-Gly-|-Ile-36 in the propeptide of collagenase 3 and 341-Asn-|-Phe-342, 441-Asp-|-Leu-442 and 354-Gln-|-Thr-355 in the aggrecan interglobular domain.
 CC -|- COFACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -|- TISSUE SPECIFICITY: Highly expressed in placenta, kidney, heart, lung, embryonic skeletal and periskeletal tissues.
 CC -|- DEVELOPMENTAL STAGE: Not detected before day 10.5. At day 12.5, prominently expressed in large arteries and the umbilical arteries, expressed at lower levels in the myocardium, craniofacial mesenchyme, nasal epithelium and liver capsule. At days 14.5 and 17.5, expressed in the musculoskeletal system, and

ossification areas, with continued expression in the arterial tunica media.
 CC CC -1- P1M: The precursor is cleaved by a furin endopeptidase (By similarity).
 CC CC -1- SIMILARITY: Belongs to peptidase family M10A.
 CC CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC CC -----
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC CC -----
 CC DR EMBL; X83536; CAA58520.2; -.
 CC DR EMBL; AF022432; AAB86602.1; -.
 CC DR EMBL; AF022424; AAB86602.1; JOINED.
 CC DR EMBL; AF022425; AAB86602.1; JOINED.
 CC DR EMBL; AF022426; AAB86602.1; JOINED.
 CC DR EMBL; AF022427; AAB86602.1; JOINED.
 CC DR EMBL; AF022428; AAB86602.1; JOINED.
 CC DR EMBL; AF022429; AAB86602.1; JOINED.
 CC DR EMBL; AF022430; AAB86602.1; JOINED.
 CC DR EMBL; AF022431; AAB86602.1; JOINED.
 CC DR EMBL; U54984; AAB51753.1; -.
 CC DR HSSP; P08254; 1HFS.
 CC DR MEROPS; M10.014; -.
 CC DR MGD; MGI:101900; Mmp14.
 CC DR InterPro; IPR000585; Hemopexin.
 CC DR InterPro; IPR001818; Pept_M10A_M12B.
 CC DR InterPro; IPR006025; Pept_M_Zn_BS.
 CC DR InterPro; IPR006026; Peptidase_M.
 CC DR Pfam; PF00045; hemopexin; 4.
 CC DR Pfam; PF00413; Peptidase_M10; 1.
 CC DR Pfam; PF03933; Peptidase_M10_N; 1.
 CC DR PRINTS; PR00138; MATRIXIN.
 CC DR SMART; SM00120; HX; 4.
 CC DR SMART; SM00235; ZnMc; 1.
 CC DR PROSITE; PS00024; HEMOPEXIN; 1.
 CC DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 CC KW Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium; Signal;
 CC Transmembrane; Collagen degradation; Extracellular matrix.
 CC FT SIGNAL 1 20
 CC FT CHAIN 21 111
 CC FT CHAIN 112 582
 CC FT DOMAIN 112 541
 CC FT TRANSMEM 542 562
 CC FT DOMAIN 563 582
 CC FT DOMAIN 316 511
 CC FT SITE 93 93
 CC FT METAL 239 239
 CC FT ACT_SITE 240 240
 CC FT METAL 243 243
 CC FT METAL 249 249
 CC FT METAL 319 508
 CC FT DISULFID 133 133
 CC FT CONFLICT 255 255
 CC FT CONFLICT 258 258
 CC FT CONFLICT 341 341
 CC FT CONFLICT 346 346
 CC FT CONFLICT 378 378
 CC FT CONFLICT 390 391
 CC FT CONFLICT 400 401
 CC FT CONFLICT 407 407
 CC FT CONFLICT 412 412
 CC FT CONFLICT 417 417
 CC FT CONFLICT 512 512
 CC SQ SEQUENCE 582 AA; 65935 MW; 3AB355156DADD175 CRC64;
 CC -----
 CC CC Query Match 5.8%; Score 8; DB 1; Length 582;
 CC CC Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LPVLLLLL 14
 Db 544 LPVLLLLL 551
 RESULT 15
 MM14 RABIT STANDARD; PRT; 582 AA.
 ID WM14 RABIT STANDARD; PRT; 582 AA.
 AC Q95220; P79225;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)
 DE Membrane-type matrix metalloproteinase 1 (MT-MMP 1) (MTMMP1)
 DE Membrane-type-1 matrix metalloproteinase (MT1-MMP) (MT1MMP).
 GN MMP14.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Vascular smooth muscle;
 RA Wang H., Keiser J.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-572 FROM N.A.
 RC STRAIN=New Zealand white;
 RA Sato T.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Seems to specifically activate progelatinase A. May thus trigger invasion by tumor cells by activating progelatinase A on the tumor cell surface (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endopeptidase activity. Activates progelatinase A by cleavage of the propeptide at 37-Asn-Leu-38. Other bonds hydrolyzed include 35-Gly-Ile-36 in the propeptide of collagenase 3, and 341-Asn-Phe-342, 441-Asp-Leu-442 and 354-Gln-Thr-355 in the aggrecan interglobular domain.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to peptidase family M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC CC -----
 CC DR EMBL; U83918; AAB41500.1; -.
 CC DR EMBL; U73940; AAD13803.1; -.
 CC DR HSSP; P08254; 1HFS.
 CC DR MEROPS; M10.014; -.
 CC DR InterPro; IPR000585; Hemopexin.
 CC DR InterPro; IPR001818; Pept_M10A_M12B.
 CC DR InterPro; IPR006025; Pept_M_Zn_BS.
 CC DR InterPro; IPR006026; Peptidase_M.
 CC DR Pfam; PF00045; hemopexin; 4.
 CC DR Pfam; PF00413; Peptidase_M10; 1.
 CC DR PRINTS; PR00138; MATRIXIN.
 CC DR SMART; SM00120; HX; 4.
 CC DR SMART; SM00235; ZnMc; 1.
 CC DR PROSITE; PS00024; HEMOPEXIN; 1.
 CC DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 CC KW Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium; Signal;
 CC Transmembrane.
 CC FT SIGNAL 1 20
 CC FT CHAIN 21 111
 CC FT CHAIN 112 582
 CC FT DOMAIN 112 541
 CC FT TRANSMEM 542 562
 CC FT DOMAIN 563 582
 CC FT DOMAIN 316 511
 CC FT SITE 93 93
 CC FT METAL 239 239
 CC FT ACT_SITE 240 240
 CC FT METAL 243 243
 CC FT METAL 249 249
 CC FT METAL 319 508
 CC FT DISULFID 133 133
 CC FT CONFLICT 255 255
 CC FT CONFLICT 258 258
 CC FT CONFLICT 341 341
 CC FT CONFLICT 346 346
 CC FT CONFLICT 378 378
 CC FT CONFLICT 390 391
 CC FT CONFLICT 400 401
 CC FT CONFLICT 407 407
 CC FT CONFLICT 412 412
 CC FT CONFLICT 417 417
 CC FT CONFLICT 512 512
 CC SQ SEQUENCE 582 AA; 65935 MW; 3AB355156DADD175 CRC64;

Wed Feb 25 11:56:33 2004

FT PROPEP 21
FT CHAIN 112 582
FT DOMAIN 112 541
FT TRANSMEM 542 562
FT DOMAIN 563 582
FT DOMAIN 316 511
FT SITE 93
FT METAL 239 239
FT ACT SITE 240 240
FT METAL 243 243
FT METAL 249 249
FT DISULFID 319 508
FT CONFLICT 29 29
FT CONFLICT 268 268
FT CONFLICT 270 270
FT CONFLICT 275 275
FT CONFLICT 292 296
FT CONFLICT 298 300
FT CONFLICT 302 308
FT CONFLICT 310 310
FT CONFLICT 317 317
FT CONFLICT 329 329
FT CONFLICT 360 360
SQ SEQUENCE 582 AA; 65963 MW; 844624B0AF1B6812 CRC64;

Query Match 5.8%; Score 8; DB 1; Length 582;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVLLLLL 14
| | | | |
Db 544 LPVLLLLL 551

Search completed: February 25, 2004, 05:10:52
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:02:27 ; Search time 23 Seconds
(without alignments)
307.511 Million cell updates/sec

Title: US-10-023-282-310
Perfect score: 725
Sequence: 1 MRTGPGPLVLLLLLAGAPAA.....CNALEYPIPTVTVLDPDRPX 137

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	724	99.9	137	4	US-09-205-258-310 Sequence 310, Appl
2	80	11.0	177	4	US-09-621-976-3938 Sequence 3938, Ap
3	74.5	10.3	174	3	US-09-383-586-12 Sequence 12, Appl
4	73	10.1	113	4	US-08-816-772-2 Sequence 2, Appli
5	72.5	10.0	294	4	US-09-322-409-7 Sequence 7, Appli
6	72.5	10.0	294	4	US-09-451-527-7 Sequence 7, Appli
7	71.5	9.9	254	4	US-09-252-991A-17480 Sequence 17480, A
8	71	9.8	378	1	US-08-133-038A-2 Sequence 2, Appli
9	71	9.8	378	1	US-08-161-988A-2 Sequence 2, Appli
10	71	9.8	679	2	US-07-998-973A-15 Sequence 15, Appl
11	71	9.8	679	2	US-08-452-800-15 Sequence 15, Appl
12	71	9.8	679	4	US-09-636-215-776 Sequence 776, App
13	71	9.8	679	4	US-09-685-166A-776 Sequence 776, App
14	71	9.8	679	5	PCT-US92-11353-15 Sequence 15, Appl
15	71	9.8	684	4	US-09-636-215-775 Sequence 775, App
16	71	9.8	684	4	US-09-685-166A-775 Sequence 775, App
17	69	9.5	327	1	US-08-420-235B-35 Sequence 35, Appl
18	69	9.5	327	3	US-08-793-624-35 Sequence 35, Appl
19	69	9.5	327	5	PCT-US95-10194-35 Sequence 35, Appl
20	69	9.5	855	4	US-09-206-551-11 Sequence 11, Appl
21	69	9.5	855	4	US-09-206-551-12 Sequence 12, Appl
22	68	9.4	382	4	US-09-542-733-2 Sequence 2, Appli
23	68	9.4	382	4	US-09-169-205D-21 Sequence 21, Appl
24	68	9.4	383	1	US-08-196-989B-4 Sequence 4, Appli
25	68	9.4	383	2	US-08-760-936-4 Sequence 4, Appli
26	68	9.4	383	4	US-09-225-024-4 Sequence 4, Appli
27	67	9.2	372	1	US-08-278-729A-33 Sequence 33, Appl

28	67	9.2	372	1	US-08-155-343A-33 Sequence 33, Appl
29	67	9.2	372	1	US-08-406-672-33 Sequence 33, Appl
30	67	9.2	372	1	US-08-643-563A-33 Sequence 33, Appl
31	67	9.2	372	1	US-08-643-563A-33 Sequence 33, Appl
32	67	9.2	372	1	US-08-462-623-33 Sequence 33, Appl
33	67	9.2	372	1	US-08-451-953A-33 Sequence 33, Appl
34	67	9.2	372	1	US-08-459-346-15 Sequence 15, Appl
35	67	9.2	372	2	US-08-445-468A-33 Sequence 33, Appl
36	67	9.2	372	2	US-08-461-397A-33 Sequence 33, Appl
37	67	9.2	372	2	US-08-512-088-33 Sequence 33, Appl
38	67	9.2	372	3	US-08-278-730A-33 Sequence 33, Appl
39	67	9.2	372	3	US-08-889-419-15 Sequence 15, Appl
40	67	9.2	372	3	US-08-445-467-33 Sequence 33, Appl
41	67	9.2	372	3	US-08-480-515A-33 Sequence 33, Appl
42	67	9.2	372	4	US-09-170-936-33 Sequence 33, Appl
43	67	9.2	372	4	US-08-402-542-15 Sequence 15, Appl
44	67	9.2	372	4	US-08-461-113-33 Sequence 33, Appl
45	67	9.2	372	4	US-08-456-033-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-205-258-310
; Sequence 310, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

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; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 310
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (137)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-310

Query Match          99.9%; Score 724; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 7.9e-79;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTGPGPLVLLLLIAGAPAAPPTPTCYSRMRALSQBITRDFNLLQVSESEPCVYLPR 60
DB 1 MRTGPGPLVLLLLIAGAPAAPPTPTCYSRMRALSQBITRDFNLLQVSESEPCVYLPR 60

QY 61 LYLDHNYCVLDKLRDFVSPPCWKVAQVDSLKDKARKLYTINMSFCRRDLVFLDDCNA 120
DB 61 LYLDHNYCVLDKLRDFVSPPCWKVAQVDSLKDKARKLYTINMSFCRRDLVFLDDCNA 120

QY 121 LEYPIPTVTLPRDQR 136
DB 121 LEYPIPTVTLPRDQR 136

RESULT 2
US-09-621-976-3938
; Sequence 3938, Application US/09621976
; Patent No. 6639063

; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3938
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -32...-1
US-09-621-976-3938

Query Match          11.0%; Score 80; DB 4; Length 177;
Best Local Similarity 25.5%; Pred. No. 0.12;
Matches 39; Conservative 13; Mismatches 29; Indels 72; Gaps 8;

QY 5 GELPVLLLL-----LAGA-----PAAPPTPP-----TCYSRMRALSQBITRDFNL-LOVSE--- 49
DB 7 GALPLCLLLPPRPLGAVSLSPARPPPPQPLPCLSRCRANCWSLLRCCTLSLTISSCP 66
QY 50 PSEPC-----VRYLPRVLDIHNVCVL 71
DB 67 PPPPLPRNAKSRPRKPKERRRHGLGAREAGASRENGEVKPLPR----- 115
QY 72 DKLRDFVASPPCCKVAQVDSLKDKARKLYTINM 104
DB 116 DKIKD-----KIKERDKERKKKKKWN 140

RESULT 3
US-09-383-586-12
; Sequence 12, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; TITLE OF INVENTION: and methods for their use
; FILE REFERENCE: 11000.1037c1
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Mouse
US-09-383-586-12

Query Match          10.3%; Score 74.5; DB 3; Length 174;
Best Local Similarity 32.9%; Pred. No. 0.52;
Matches 25; Conservative 9; Mismatches 37; Indels 5; Gaps 2;

QY 9 VLLLLIAGAPAAPPTPTCYSRMRALSQBITRDFNLLQVSESEPCVYLPRVLDIHN 68
DB 19 VLLLLISGASAOEPFPRVGCSEYTNRSCECLRNVSCLWCNE--NACMDIPVRKILPASL 77
QY 69 CVLDKLRDFVASPPCW 84
DB 78 CKLSSARWGV-----CW 89
```

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```
RESULT 4
US-08-816-772-2
; Sequence 2, Application US/08816772
; Patent No. 6410268
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: LI, HAODONG
; APPLICANT: SU, JEFFREY
; TITLE OF INVENTION: CHEMOKINE ALPHA-3
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,772
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0980001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-772-2

Query Match 10.1%; Score 73; DB 4; Length 113;
Best Local Similarity 32.3%; Pred. No. 0.44;
Matches 32; Conservative 9; Mismatches 30; Indels 28; Gaps 4;

QY 2 RTPGP-----LPVLLLLLAGAPAAAPTPTTCYSRMRALSOEITRDFNLLQVSESEPCV 55
Db 10 RVPGSGSLCALLALLL-----TPPGLAGAGPVSALT-----ELRCTCL 52

QY 56 RYLRLYLIDHNYCVDKLRDFVAPPCWKVAQVDSLKD 94
Db 53 RVTLRV-----NPKTIGKLQVFPAPQCSKVEVVASLKN 86

RESULT 5
US-09-322-409-7
; Sequence 7, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7

Query Match 10.1%; Score 73; DB 4; Length 113;
Best Local Similarity 32.3%; Pred. No. 0.44;
Matches 32; Conservative 9; Mismatches 30; Indels 28; Gaps 4;

QY 2 RTPGP-----LPVLLLLLAGAPAAAPTPTTCYSRMRALSOEITRDFNLLQVSESEPCV 55
Db 10 RVPGSGSLCALLALLL-----TPPGLAGAGPVSALT-----ELRCTCL 52

QY 56 RYLRLYLIDHNYCVDKLRDFVAPPCWKVAQVDSLKD 94
Db 53 RVTLRV-----NPKTIGKLQVFPAPQCSKVEVVASLKN 86

RESULT 6
US-09-451-527-7
; Sequence 7, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7

Query Match 10.0%; Score 72.5; DB 4; Length 294;
Best Local Similarity 22.4%; Pred. No. 1.8;
Matches 38; Conservative 24; Mismatches 57; Indels 51; Gaps 8;

QY 6 PLPVLILLLAGAPAAAPTPTTCYSR-----MRALSOEITRDFNLLQVS--EPSEP 53
Db 10 PTASLILLLLSPGLRGTPDCSFHSPISTFAVTIRKLSYLLQDYPTVTASNLQDDEL 69

QY 54 C-----VRYLPRLY-----LDIH--NYCVDKLRDFVAPPCWKVA 87
Db 70 CGAFWRLVLAQRWVRLQVAGSQMILLLEAVNTEIHFTVTCFAQPL-----PSCLRFV 123

QY 88 QVD---SLKDKARKLYTIMNSFCRRDLVFLDDCNALIEYPIPTVTVLDPDR 134
Db 124 QTNISHLQDTSQQLAALKPWITRRN----FSGCLELQCPDSSSTLVPPR 169

RESULT 7
US-09-252-991A-17480
; Sequence 17480, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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; LENGTH: 294
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-7

Query Match 10.0%; Score 72.5; DB 4; Length 294;
Best Local Similarity 22.4%; Pred. No. 1.8;
Matches 38; Conservative 24; Mismatches 57; Indels 51; Gaps 8;

QY 6 PLPVLILLLAGAPAAAPTPTTCYSR-----MRALSOEITRDFNLLQVS--EPSEP 53
Db 10 PTASLILLLLSPGLRGTPDCSFHSPISTFAVTIRKLSYLLQDYPTVTASNLQDDEL 69

QY 54 C-----VRYLPRLY-----LDIH--NYCVDKLRDFVAPPCWKVA 87
Db 70 CGAFWRLVLAQRWVRLQVAGSQMILLLEAVNTEIHFTVTCFAQPL-----PSCLRFV 123

QY 88 QVD---SLKDKARKLYTIMNSFCRRDLVFLDDCNALIEYPIPTVTVLDPDR 134
Db 124 QTNISHLQDTSQQLAALKPWITRRN----FSGCLELQCPDSSSTLVPPR 169

RESULT 6
US-09-451-527-7
; Sequence 7, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7

Query Match 10.0%; Score 72.5; DB 4; Length 294;
Best Local Similarity 22.4%; Pred. No. 1.8;
Matches 38; Conservative 24; Mismatches 57; Indels 51; Gaps 8;

QY 6 PLPVLILLLAGAPAAAPTPTTCYSR-----MRALSOEITRDFNLLQVS--EPSEP 53
Db 10 PTASLILLLLSPGLRGTPDCSFHSPISTFAVTIRKLSYLLQDYPTVTASNLQDDEL 69

QY 54 C-----VRYLPRLY-----LDIH--NYCVDKLRDFVAPPCWKVA 87
Db 70 CGAFWRLVLAQRWVRLQVAGSQMILLLEAVNTEIHFTVTCFAQPL-----PSCLRFV 123

QY 88 QVD---SLKDKARKLYTIMNSFCRRDLVFLDDCNALIEYPIPTVTVLDPDR 134
Db 124 QTNISHLQDTSQQLAALKPWITRRN----FSGCLELQCPDSSSTLVPPR 169

RESULT 7
US-09-252-991A-17480
; Sequence 17480, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17480
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17480

Query Match 9.8%; Score 71.5; DB 4; Length 254;
Best Local Similarity 21.2%; Pred. No. 2;
Matches 29; Conservative 22; Mismatches 59; Indels 27; Gaps 4;

QY 4 PGPLVLLLLAGAPAAARPTPTCYSRMRALSQETITDFNLLQVSEPCVRLPRLYL 63
Db 121 PGCKPYAEAAG-DKINKCPGGEATIRALADLLDLEPFLDAEETPRVAYI----- 174
QY 64 DIHNYCVLDKLRDFVAPPCWQVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALAY 123
Db 175 -----REARCIGCTGCTIOACVPDAIVGAARLMTHTVIADEC-----TGCDLCLE 217
QY 124 PIPVTVT-----LPDROR 136
Db 218 PCVPDCIEMREIPDVR 234

RESULT 8
US-08-133-038A-2
; Sequence 2, Application US/08133038A
; Patent No. 5541063
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Toshio
; TITLE OF INVENTION: SUBUNIT OF THE HUMAN INTERLEUKIN-3 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940-1000

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System Software 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,038A
FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03026
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,355
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0141Q
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IL-3-receptor
US-08-133-038A-2

Query Match 9.8%; Score 71; DB 1; Length 378;
Best Local Similarity 20.3%; Pred. No. 3.9;
Matches 25; Conservative 13; Mismatches 37; Indels 48; Gaps 3;

QY 10 LLLLLAGAPA-----ARPTPTCYSRMRALSQETITDFNLLQVSEPCVRLPRLYL 64
Db 6 LTLALLALPCLLQTKEDPNPPTNLKMKAKAQAQLTWDLR----- 45
QY 65 IHNYCVLDKLRDFVAPPCWQVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALAY 124
Db 46 -----NVTDICVADADYSMPAVANSYCFGAISL---CEVTNT 82
QY 125 IPV 127
Db 83 VRV 85

RESULT 9
US-08-161-988A-2
; Sequence 2, Application US/08161988A
; Patent No. 5639605
; GENERAL INFORMATION:
; APPLICANT: Kitamura, Toshio
; APPLICANT: Miyajima, Aetsushi
; TITLE OF INVENTION: HUMAN INTERLEUKIN-3 RECEPTOR COMPONENT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,988A
FILING DATE: 03-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,355
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0141Q1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-161-988A-2

Query Match 9.8%; Score 71; DB 1; Length 378;
Best Local Similarity 20.3%; Pred. No. 3.9;
Matches 25; Conservative 13; Mismatches 37; Indels 48; Gaps 3;

QY 10 LLLLLAGAPA-----ARPTPTCYSRMRALSQETITDFNLLQVSEPCVRLPRLYL 64
Db 6 LTLALLALPCLLQTKEDPNPPTNLKMKAKAQAQLTWDLR----- 45
QY 65 IHNYCVLDKLRDFVAPPCWQVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALAY 124
Db 46 -----NVTDICVADADYSMPAVANSYCFGAISL---CEVTNT 82
QY 125 IPV 127
Db 83 VRV 85

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Db 6 LTLIALPCLLOTKEDPNPITNLRMKAKAQLTWDLNR----- 45
QY 65 IHNYCVLDKLRDFVSPCKWQVDSLKDKARKLYTINMSFCRDLVFLDDCNALVYP 124
Db 46 -----NVTDIKCVKADYSPVANNVSYCQFGAISL---CEVTNYT 82
QY 125 IPV 127
Db 83 VRV 85

RESULT 10
US-07-998-973A-15
; Sequence 15, Application US/07998973A
; Patent No. 5514579
; GENERAL INFORMATION:
; APPLICANT: O'Hara, Patrick J
; APPLICANT: Grant, Francis J
; APPLICANT: Sheppard, Paul O
; TITLE OF INVENTION: NOVEL HUMAN TRANSGLUTAMINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/998,973A
; FILING DATE: 19921230
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,284
; FILING DATE: 31-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steve W
; REGISTRATION NUMBER: 31-990
; REFERENCE/DOCKET NUMBER: 13952-13-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 206-623-6793
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-998-973A-15

Query Match 9.8%; Score 71; DB 1; Length 679;
Best Local Similarity 21.8%; Pred. No. 8.5;
Matches 22; Conservative 16; Mismatches 39; Indels 24; Gaps 2;

QY 23 TPPTCYSMRALSQBITRDFNLQVSEPCVRYLPRLYLDIHNYCVLDKLRDFVSP 82
Db 82 TPSDHYNQATLQNESGKEVTAVTSSPAILGKY--QLNVKTGNHI----- 126
QY 83 CWKVAQVDSLKDKARKLYTINMSFCRDLVFLDDCNALV 123
Db 127 -----LKSEENILYLFNPCKEDWFMPEDEKEY 158

RESULT 11
US-08-452-800-15
; Sequence 15, Application US/08452800
; Patent No. 5952011
; GENERAL INFORMATION:
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; APPLICANT: O'Hara, Patrick J
; APPLICANT: Grant, Francis J
; APPLICANT: Sheppard, Paul O
; TITLE OF INVENTION: NOVEL HUMAN TRANSGLUTAMINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,800
; FILING DATE: 30-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/998,973
; FILING DATE: 30-DEC-1992
; APPLICATION NUMBER: US 07/816,284
; FILING DATE: 31-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steve W
; REGISTRATION NUMBER: 31-990
; REFERENCE/DOCKET NUMBER: 13952-13-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 206-623-6793
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-452-800-15

Query Match 9.8%; Score 71; DB 2; Length 679;
Best Local Similarity 21.8%; Pred. No. 8.5;
Matches 22; Conservative 16; Mismatches 39; Indels 24; Gaps 2;

QY 23 TPPTCYSMRALSQBITRDFNLQVSEPCVRYLPRLYLDIHNYCVLDKLRDFVSP 82
Db 82 TPSDHYNQATLQNESGKEVTAVTSSPAILGKY--QLNVKTGNHI----- 126
QY 83 CWKVAQVDSLKDKARKLYTINMSFCRDLVFLDDCNALV 123
Db 127 -----LKSEENILYLFNPCKEDWFMPEDEKEY 158

RESULT 12
US-09-636-215-776
; Sequence 776, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
```

```

; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636.215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-776

Query Match          9.8%; Score 71; DB 4; Length 679;
Best Local Similarity 21.8%; Pred. No. 8.5;
Matches 22; Conservative 16; Mismatches 39; Indels 24; Gaps 2;

QY 23 TPPTCYSRMRALSQETTRDFNLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDFVASPP 82
Db 82 TPSDHYNQWATLQNESGKEVTAVTSSPNAILGKY--QLNVKTGNHI----- 126

QY 83 CWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALEY 123
Db 127 -----LKSEENILYLLFNPWCKEDMVFMPDEDERKEY 158

RESULT 13
US-09-685-166A-776
; Sequence 776, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-776

Query Match          9.8%; Score 71; DB 4; Length 679;
Best Local Similarity 21.8%; Pred. No. 8.5;
Matches 22; Conservative 16; Mismatches 39; Indels 24; Gaps 2;

QY 23 TPPTCYSRMRALSQETTRDFNLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDFVASPP 82
Db 82 TPSDHYNQWATLQNESGKEVTAVTSSPNAILGKY--QLNVKTGNHI----- 126

QY 83 CWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALEY 123
Db 127 -----LKSEENILYLLFNPWCKEDMVFMPDEDERKEY 158
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Db 127 -----LKSEENILYLLFNPWCKEDMVFMPDEDERKEY 158

RESULT 14
PCT-US92-11353-15
; Sequence 15, Application PC/TUS9211353
; GENERAL INFORMATION:
; APPLICANT: O'Hara, Patrick J
; APPLICANT: Grant, Francis J
; APPLICANT: Sheppard, Paul O
; TITLE OF INVENTION: NOVEL HUMAN TRANSGLUTAMINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11353
; FILING DATE: 19921230
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,284
; FILING DATE: 31-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steve W
; REGISTRATION NUMBER: 31-990
; REFERENCE/DOCKET NUMBER: 13952-13-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 206-623-6793
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-11353-15

Query Match          9.8%; Score 71; DB 5; Length 679;
Best Local Similarity 21.8%; Pred. No. 8.5;
Matches 22; Conservative 16; Mismatches 39; Indels 24; Gaps 2;

QY 23 TPPTCYSRMRALSQETTRDFNLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDFVASPP 82
Db 82 TPSDHYNQWATLQNESGKEVTAVTSSPNAILGKY--QLNVKTGNHI----- 126

QY 83 CWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALEY 123
Db 127 -----LKSEENILYLLFNPWCKEDMVFMPDEDERKEY 158

RESULT 15
US-09-636-215-775
; Sequence 775, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
```



```
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 775
; LENGTH: 684
; TYPE: FRT
; ORGANISM: Homo sapiens
US-09-636-215-775
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Query Match          9.8%; Score 71; DB 4; Length 684;
Best Local Similarity 21.8%; Pred. No. 8.6;
Matches 22; Conservative 16; Mismatches 39; Indels 24; Gaps 2;

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Db      82  TPSDHYNQATLQNESGKEVTVAVTSSPNAILGKY--QLNVKTGNHI----- 126

QY      83  CWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALRY 123
      |||  :  ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      127  -----LKSEENILYLLFNFPCKEDWVMPDEDERKEY 158
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Search completed: February 25, 2004, 05:04:48
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2004, 05:04:17 ; Search time 33 Seconds
(without alignments)
876.606 Million cell updates/sec

Title: US-10-023-282-310
Perfect score: 725
Sequence: 1 MKTPGPLPVLLLLLAGAPAA.....CNALXPPIPVTTVLPRQXK 137

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	724	99.9	136	13	US-10-036-342-65
3	724	99.9	136	13	US-10-036-041-65
4	724	99.9	136	14	US-10-036-855-65
5	724	99.9	136	14	US-10-036-214-65
6	724	99.9	136	14	US-10-036-719-65
7	724	99.9	136	14	US-10-036-160-65
8	724	99.9	136	14	US-10-020-419-2
9	724	99.9	136	14	US-10-035-958-65
10	724	99.9	136	14	US-10-036-150-65
11	724	99.9	136	14	US-10-036-063-65
12	724	99.9	136	14	US-10-036-063-65
13	724	99.9	136	14	US-10-223-085-312
14	724	99.9	136	14	US-10-223-084-312
15	724	99.9	136	14	US-10-223-088-312

16	724	99.9	136	14	US-10-223-090-312
17	724	99.9	136	14	US-10-223-087-312
18	724	99.9	136	14	US-10-223-083-312
19	724	99.9	136	14	US-10-223-089-312
20	724	99.9	136	14	US-10-035-977-65
21	724	99.9	136	14	US-10-223-081-312
22	724	99.9	136	14	US-10-223-082-312
23	724	99.9	137	10	US-09-933-767-310
24	724	99.9	137	14	US-10-023-282-310
25	601	82.9	112	10	US-09-933-767-1245
26	484	66.8	139	14	US-10-213-288-4
27	479	66.1	136	14	US-10-020-419-4
28	88	12.1	557	13	US-10-044-205A-13
29	75	10.3	114	15	US-10-295-027-464
30	75	10.3	114	15	US-10-295-027-464
31	75	10.3	615	10	US-09-858-909-2
32	75	10.3	615	14	US-10-172-712-30
33	74.5	10.3	174	9	US-09-823-038A-12
34	74.5	10.3	174	15	US-10-108-260A-4760
35	73.5	10.1	283	14	US-10-161-051-140
36	72.5	10.0	294	14	US-10-218-654-7
37	72.5	10.0	294	14	US-10-262-439-7
38	72.5	10.0	549	13	US-10-044-205A-14
39	71	9.8	419	15	US-10-369-493-3032
40	71	9.8	566	9	US-09-925-297-668
41	71	9.8	679	9	US-09-759-143-776
42	71	9.8	679	9	US-09-780-669-776
43	71	9.8	679	9	US-09-822-827-776
44	71	9.8	679	9	US-09-895-793-776
45	71	9.8	679	9	US-09-895-793-776

ALIGNMENTS

RESULT 1

US-09-931-836-65
; Sequence 65, Application US/09931836
; Publication No. US20030027249A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C1
; CURRENT APPLICATION NUMBER: US/09/931.836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22

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; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-931-836-65

Query Match          99.9%; Score 724; DB 10; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTPGPLPVLILLLAGAAPRPTPTCYSMRALSQBITDFNLLQVSESEPCVRLPR 60
DB 1 MRTPGPLPVLILLLAGAAPRPTPTCYSMRALSQBITDFNLLQVSESEPCVRLPR 60
QY 61 LYLDIHNVCYLDKLRDFVASPPCKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
DB 61 LYLDIHNVCYLDKLRDFVASPPCKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
QY 121 LEYPIPVTVTLPRQR 136
DB 121 LEYPIPVTVTLPRQR 136

RESULT 2
US-10-036-342-65
; Sequence 65, Application US/10036342
; Publication No. US20020090681A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C5
; CURRENT APPLICATION NUMBER: US/10/036,342
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23

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; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131272
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
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; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264

; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
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; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-342-65

Query Match 99.9%; Score 724; DB 13; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTGPLPVLILLGAPAAARTPTTCYSRMALSOEITRDNLQVSPSPCVRYLPR 60
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Db 1 MPTGPLPVLILLGAPAAARTPTTCYSRMALSOEITRDNLQVSPSPCVRYLPR 60
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QY 61 LYLDHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTIMNSFCRDLLVLLDDCNA 120
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Db 61 LYLDHNYCVLDKLRDFVASPCWKVAQVDSLKDKARKLYTIMNSFCRDLLVLLDDCNA 120
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QY 121 LEYPIPTVTVLPDROR 136
|||
Db 121 LEYPIPTVTVLPDROR 136
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RESULT 3

US-10-036-041-65
; Sequence 65, Application US/10036041
; Publication NO. US20020192751A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C8
; CURRENT APPLICATION NUMBER: US/10/036,041
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23

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US-101-035-855-65
/ Sequence 65, Application US/10035855
/ Publication No. US20030008348A1
/ GENERAL INFORMATION:
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRADE
/ TITLE OF INVENTION: ACIDS ENCODING
/ FILE REFERENCE: F3030R1C4
/ CURRENT APPLICATION NUMBER: US/10/035855
/ PRIOR FILING DATE: 2001-12-26
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/112514
/ PRIOR FILING DATE: 1998-12-15
/ PRIOR APPLICATION NUMBER: 60/113300
/ PRIOR FILING DATE: 1998-12-22

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/ APPLICANT: zhang, zemin
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / TITLE OF INVENTION: ACIDS ENCODING THE SAME
 / FILE REFERENCE: P3030R1C4
 / CURRENT APPLICATION NUMBER: US/10/035,855
 / CURRENT FILING DATE: 2001-12-26
 / PRIOR APPLICATION NUMBER: 60/085579
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/112514
 / PRIOR FILING DATE: 1998-12-15
 / PRIOR APPLICATION NUMBER: 60/113300
 / PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
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; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
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; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
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; PRIOR APPLICATION NUMBER: 60/131291
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; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
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; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
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; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
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; PRIOR FILING DATE: 1999-05-14
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; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908, 827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
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; PRIOR APPLICATION NUMBER: PCT/US99/30720

; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-035-855-65

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTGGLPVLILLLAGAPAAAPTPTCYSRMRALSQETTRDFNLLQVSEPCVRYLPR 60
Db 1 MRTGGLPVLILLLAGAPAAAPTPTCYSRMRALSQETTRDFNLLQVSEPCVRYLPR 60
QY 61 LYLDIHNVCVLDKLRDFVASPPCKWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
Db 61 LYLDIHNVCVLDKLRDFVASPPCKWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
QY 121 LEYPIPTVTTLVLPDRQR 136
Db 121 LEYPIPTVTTLVLPDRQR 136

RESULT 5

US-10-036-214-65
; Sequence 65, Application US/10036214
; Publication No. US20030032061A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030RIC11
; CURRENT APPLICATION NUMBER: US/10/036,214
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15


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; CURRENT APPLICATION NUMBER: US/10/035,719
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/113605
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; PRIOR APPLICATION NUMBER: 09/816744
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; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599

; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15364
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
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; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-035-719-65

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTGPLEVILLILLAGAPAAAPTPTCYSRMRALSQEIITRDFNLLQVSEPPCYVYLP 60
DB 1 MRTGPLEVILLILLAGAPAAAPTPTPTCYSRMRALSQEIITRDFNLLQVSEPPCYVYLP 60
QY 61 LYLDIHNYCVLDKLRDFVASPPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
DB 61 LYLDIHNYCVLDKLRDFVASPPCKWVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
QY 121 LEYPIPTVTLVLPDROR 136
DB 121 LEYPIPTVTLVLPDROR 136

RESULT 7
US-10-036-160-65
; Sequence 65, Application US/10036160
; Publication No. US20030044842A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
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APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P30301C3
; CURRENT APPLICATION NUMBER: US/10/036,160
; CURRENT FILING DATE: 2001-12-26
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 65
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-160-65

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRTPGPLPVLILLIAGAPAAARPTPTCYSRMRALSQBITRDFNLLQVSEPCVYLPR 60
Db 1 MRTPGPLPVLILLIAGAPAAARPTPTCYSRMRALSQBITRDFNLLQVSEPCVYLPR 60
Qy 61 LYLDIHNKCYLDKLDKDFVSPPCWKAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Db 61 LYLDIHNKCYLDKLDKDFVSPPCWKAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Qy 121 LEYPIPVTTVLPRQR 136
Db 121 LEYPIPVTTVLPRQR 136
RESULT 8
US-10-020-419-2
; Sequence 2, Application US/10020419
; Publication No. US20030044897A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; APPLICANT: Ye, Weilan
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: NOVEL SECRETED POLYPEPTIDE AND METHODS OF TREATMENT OF

;; TITLE OF INVENTION: BONE DISORDERS
;; FILE REFERENCE: P2637-1(US)
;; CURRENT APPLICATION NUMBER: US/10/020,419
;; CURRENT FILING DATE: 2001-12-13
;; PRIOR APPLICATION NUMBER: US 60/132,379
;; PRIOR FILING DATE: 1999-05-04
;; PRIOR APPLICATION NUMBER: PCT/US00/05601
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-03
;; NUMBER OF SEQ ID NOS: 4
;; SEQ ID NO 2
;; LENGTH: 136
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-020-419-2

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRTGPLPVLLLLAGAPARTPTTCYSRMALSQEITRDNLLQVSEPPSPCVRYLPR 60
Db 1 MRTGPLPVLLLLAGAPARTPTTCYSRMALSQEITRDNLLQVSEPPSPCVRYLPR 60
Qy 61 LYLDHNYCVLDKDFVASPPCKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Db 61 LYLDHNYCVLDKDFVASPPCKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA 120
Qy 121 LEYPIPTVTLPRDR 136
Db 121 LEYPIPTVTLPRDR 136

RESULT 9
US-10-035-958-65
;; Sequence 65, Application US/10035958
;; Publication NO. US20030049733A1
;; GENERAL INFORMATION:
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3030R1C7
;; CURRENT APPLICATION NUMBER: US/10/035,958
;; CURRENT FILING DATE: 2001-12-26
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/112514
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113300
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/113430
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113605
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/114140
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115552
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/116843

;; PRIOR FILING DATE: 1999-01-22
;; PRIOR APPLICATION NUMBER: 60/125774
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/125778
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/125826
;; PRIOR FILING DATE: 1999-03-24
;; PRIOR APPLICATION NUMBER: 60/127035
;; PRIOR FILING DATE: 1999-03-31
;; PRIOR APPLICATION NUMBER: 60/127706
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/129122
;; PRIOR FILING DATE: 1999-04-13
;; PRIOR APPLICATION NUMBER: 60/130359
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/131270
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131272
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/132371
;; PRIOR FILING DATE: 1999-05-04
;; PRIOR APPLICATION NUMBER: 60/132379
;; PRIOR FILING DATE: 1999-05-04
;; PRIOR APPLICATION NUMBER: 60/132383
;; PRIOR FILING DATE: 1999-05-04
;; PRIOR APPLICATION NUMBER: 60/135750
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/138166
;; PRIOR FILING DATE: 1999-06-08
;; PRIOR APPLICATION NUMBER: 60/144791
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/146970
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/162506
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: 09/311832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 09/380142
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/644848
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 09/747259
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: 09/816744
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: 09/854208
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: 09/854280
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: 09/874503
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: 09/869599
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: 09/908,827
;; PRIOR FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: PCT/US99/10733
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: PCT/US99/28551
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30720
;; PRIOR FILING DATE: 1999-12-22
;; PRIOR APPLICATION NUMBER: PCT/US00/05601
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23

[illegible]

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels

;
; PRIOR APPLICATION NUMBER

; PRIOR APPLICATION NUMBER: 60/131291
: PRIOR FILING DATE: 1999-04-27

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/132379
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/132383
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138166
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/146970
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
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PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 65
LENGTH: 136
TYPE: PRT
ORGANISM: Homo Sapien
US-10-036-063-65

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71; Indels 0; Gaps 0;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPGFLPVLILLAGAPAAARTPTPTCYSRMRLSQEITRDNLLQVSEPFPCVRYLPR 60
DB 1 MTPGFLPVLILLAGAPAAARTPTPTCYSRMRLSQEITRDNLLQVSEPFPCVRYLPR 60
QY 61 LYLDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTTMNSFCRDLVFLDDCNA 120
DB 61 LYLDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTTMNSFCRDLVFLDDCNA 120
QY 121 LEYPIPVTVLDRQR 136
DB 121 LEYPIPVTVLDRQR 136

RESULT 13
US-10-223-085-312
; Sequence 312, Application US/10223085
; Publication No. US20030100497A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC10
; CURRENT APPLICATION NUMBER: US/10/223,085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 312
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-085-312

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 4e-71;

RESULT 15

Query Match 99.9%; Score 724; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. NO. 4e-71;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MRTGPELVLLLLLAGAAPAAAPTPTTCYSMRALSOITDFNLLQVSEPFSEPCVAYLPR 60
Db 1 MTTGPELVLLLLLAGAAPAAAPTPTTCYSMRALSOITDFNLLQVSEPFSEPCVAYLPR 60

Wed Feb 25 11:56:34 2004

QY	61	LYLDIHNYCVLDKLRDFVASPPCKVQAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA	120
Db	61	LYLDIHNYCVLDKLRDFVASPPCKVQAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA	120
QY	121	LEYPIPVTTVLPRQR	136
Db	121	LEYPIPVTTVLPRQR	136

Search completed: February 25, 2004, 05:09:11
Job time : 34 secs


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Query Match      10.3%; Score 75; DB 1; Length 615;
Best Local Similarity 25.5%; Pred. No. 12;
Matches 26; Conservative 12; Mismatches 36; Indels 28; Gaps 5;

Qy 2 RTPGELPVLILLAGAAPARETPP-----TCYSRMRLASQEITRDFNLLQVSESEP 53
      |||||
Db 336 OTPGAL-----PAKREOPPLSTENGSLSCGQRLKRLSSMTVRVGGELVALRCAMP 385
      |||||

```

RESULT 4

B40825
hypothetical protein - vaccinia virus (strain WR)

C:Species: vaccinia virus
C:Date: 25-Sep-1992 #sequence_revision 25-Sep-1992 #text_change 08-Oct-1999
C:Accession: B40825; S29909
R:Amegadzie, B.Y.; Sisler, J.R.; Moss, B.
Virology 186, 777-782, 1992

A:Title: Frame-shift mutations within the vaccinia virus A-type inclusion protein gene.
A:Reference number: A40825; MUID:52124754; PMID:1733111

A:Accession: B40825
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-278 <AM1>
A:Cross-references: GB:M61187
R:Amegadzie, B.Y.
submitted to the EMBL Data Library, January 1991

A:Reference number: S29907
A:Accession: S29909
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-278 <AM2>

Query Match	10.0%	Score 72.5	DB 2	Length 278;
Best Local Similarity	27.1%	Pred. No. 8.6;		
Matches 35;	Conservative 13;	Mismatches 58;	Indels 23;	Gaps 6;

Query Match 9.9%; Score 72; DB 2; Length 660;
Best Local Similarity 26.7%; Pred. No. 26;
Matches 39; Conservative 19; Mismatches 60; Indels 28; Gaps 5;

QY 4 PGPLVILLIAGAPAAAPPTPTCYSRMRALSQBITRDNFLQVSESPQVYLPRLYL 63
DB 157 PKPTPI-----PEHPRPFP-----HEYHKKPLLPVEEP-DPVKKADRIKL 200
QY 64 DIHNYCVLDKLRDFVAPSPCKWKAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALAY 123
DB 201 DNHIINTLDHNLNFIH-YCCDTAAVDRLEHHIETLGQYAVILARK-----INNQTLLF 253
QY 124 PIPVTVLP 132
DB 254 FWPPLTPVHP 262

RESULT 5
D72391
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: D72391
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: D72391
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-660 <ARN>
A:Cross-references: GB:AE001713; GB:AE000512; NID:g4980809; PIDN:AAD35397.1; PID:g4980801
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0309

Query Match 9.9%; Score 72; DB 2; Length 660;
Best Local Similarity 26.7%; Pred. No. 26;
Matches 39; Conservative 19; Mismatches 60; Indels 28; Gaps 5;

QY 4 PGPLVILLIAGAPAAAPPTPTCYSRMRALSQBITRDNFLQVSESPQVYLPRLYL 63
DB 330 PGP-GVPLLENKSGG-----YRVLKWTGDSVSMVNLNISDPDPVGEVFRDVR 382
QY 57 YLPRLYLDIHNYCVLDKLRDFVAPSPCKWKAQVDSLKDKARKLYTIM 103
DB 383 FQALSLAINREINEILFNGLAEPQASVSSPYDPEWEKAYAEYDPDRANKLLDEM 442
QY 104 N-SFCRRDLVFLDDCNALAYEPIPT 128
DB 443 GLKWDSEHREYRLLPDGRPLRFTTQVT 468

RESULT 6
C83208
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83208
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83208
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <STO>
A:Cross-references: GB:AE004770; GB:AE004091; NID:g9949633; PIDN:AAG06878.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3490
C:Superfamily: conserved hypothetical protein HI1684; ferredoxin 2[4Fe-4S] homology

Query Match 9.8%; Score 71; DB 2; Length 378;
Best Local Similarity 20.3%; Pred. No. 17;
Matches 25; Conservative 13; Mismatches 37; Indels 48; Gaps 3;

QY 10 LILLIAGAPAA-----ARPTPTCYSRMRALSQBITRDNFLQVSESPQVYLPRLYL 64
DB 6 LTLILLIAPCLLTQKEDENPPITNLRMKAKAQLTWLNR----- 45
QY 65 IHNYCVLDKLRDFVAPSPCKWKAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALAY 124
DB 46 -----NVTDECVDADYSMPAVNNSYCQFGAISL-----CEVTNYT 82
QY 125 IPV 127
DB 83 VRV 85

RESULT 8
T32820
hypothetical protein F54D12.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32820
R:Maggi, L.; Goela, D.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid F54D12.
A:Reference number: Z21228
A:Accession: T32820
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-645 <WAG>
A:Cross-references: EMBL:AF040647; PIDN:AAE94990.1; GSPDB:GN00020; CESP:F54D12.7
A:Experimental source: strain Bristol N2; clone F54D12
C:Genetics:
A:Gene: CESP:F54D12.7
A:Map position: 2
A:Introns: 51/2; 129/3; 178/1; 196/3; 276/3; 297/3; 324/2; 354/3; 470/1; 503/1; 538/3;

Query Match 9.9%; Score 71.5; DB 2; Length 188;
Best Local Similarity 21.2%; Pred. No. 6.9;
Matches 29; Conservative 22; Mismatches 59; Indels 27; Gaps 4;

QY 4 PGPLVILLIAGAPAAAPPTPTCYSRMRALSQBITRDNFLQVSESPQVYLPRLYL 63
DB 55 PGCKPYAATAAG-DKINKCPGGGATIRALDLDLEPEFLDAAEETPPRVAVI----- 108
QY 64 DIHNYCVLDKLRDFVAPSPCKWKAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALAY 123
DB 109 -----REACIGCTKCIQACPDVAIVGAARLMHTVIADEC-----TGCDLCLE 151
QY 124 PIPVTV-----LPDRQR 136
DB 152 PCPVDCTEMREIPDVR 168

RESULT 7
A40266
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C:Accession: A40266
R:Kitamura, T.; Sato, N.; Arai, K.; Miyajima, A.
Cell 66, 1165-1174, 1991
A:Title: Expression cloning of the human IL-3 receptor cDNA reveals a shared beta subunit
A:Reference number: A40266; MUID:92005668; PMID:1833064
A:Accession: A40266
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <KIT>
A:Cross-references: GB:M74782; NID:g186330; PIDN:AAA59148.1; PID:g186331
C:Keywords: cytokine receptor; transmembrane protein

Query Match 9.8%; Score 71; DB 2; Length 378;
Best Local Similarity 20.3%; Pred. No. 17;
Matches 25; Conservative 13; Mismatches 37; Indels 48; Gaps 3;

QY 10 LILLIAGAPAA-----ARPTPTCYSRMRALSQBITRDNFLQVSESPQVYLPRLYL 64
DB 6 LTLILLIAPCLLTQKEDENPPITNLRMKAKAQLTWLNR----- 45
QY 65 IHNYCVLDKLRDFVAPSPCKWKAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALAY 124
DB 46 -----NVTDECVDADYSMPAVNNSYCQFGAISL-----CEVTNYT 82
QY 125 IPV 127
DB 83 VRV 85

RESULT 8
T32820
hypothetical protein F54D12.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32820
R:Maggi, L.; Goela, D.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid F54D12.
A:Reference number: Z21228
A:Accession: T32820
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-645 <WAG>
A:Cross-references: EMBL:AF040647; PIDN:AAE94990.1; GSPDB:GN00020; CESP:F54D12.7
A:Experimental source: strain Bristol N2; clone F54D12
C:Genetics:
A:Gene: CESP:F54D12.7
A:Map position: 2
A:Introns: 51/2; 129/3; 178/1; 196/3; 276/3; 297/3; 324/2; 354/3; 470/1; 503/1; 538/3;

Query Match 9.8%; Score 71; DB 2; Length 645;
 Best Local Similarity 38.5%; Pred. No. 32;
 Matches 20; Conservative 6; Mismatches 20; Indels 6; Gaps 3;

QY 14 LAGAPAAAPPTPTC--YGRMRALSOE---ITRDFNLLQVSESPFCVRLPR 60
 DB 530 LANLPSTVPVPGDCSSYPTAKFLSQOQRITYSFRTMPVSNDS-PCIRGTPTK 580

RESULT 9
 S71105
 protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) 4, prostate specific - human
 N:Alternate names: transglutaminase 4, prostate specific
 C:Species: Homo sapiens (man)
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000
 C:Accession: S71105; J02501
 R:Dubbink, H.J.; Verkaik, N.S.; Faber, P.W.; Trapman, J.; Schroeder, F.H.; Romijn, J.C.
 Biochem. J. 315, 901-908, 1996
 A:Title: Tissue-specific and androgen-regulated expression of human prostate-specific tr
 A:Reference number: S71105; MUID:96220705; PMID:8645175
 A:Accession: S71105
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-684 <DUB>
 A:Cross-references: EMBL:U31905; NID:gl353349; PIDN:AAC50516.1; PID:gl353350
 R:Grant, F.J.; Taylor, D.A.; Sheppard, P.O.; Mathewes, S.L.; Lint, W.; Vanaja, E.; Bisho
 Biochem. Biophys. Res. Commun. 203, 1117-1123, 1994
 A:Title: Molecular cloning and characterization of a novel transglutaminase cDNA from a
 A:Reference number: J02501; MUID:94380018; PMID:7916568
 A:Accession: J02501
 A:Molecule type: mRNA
 A:Residues: 1-312, 'E', 314-337, 343-465, 'Q', 467-583, 'N', 585-684 <GRA>
 A:Cross-references: GB:134840; NID:G2766555; PIDN:AAH95430.1; PID:G2766556
 A:Experimental source: prostate
 A:Note: the sequence is revised in GenBank entry HUMTGLTWN, release 113.0, PIDN:AAH95430
 C:Genetics:
 A:Gene: GDB:TGM4
 A:Cross-references: GDB:451945; OMIM:600585
 A:Map position: 3p22-3p21.33
 C:Superfamily: protein-glutamine gamma-glutamyltransferase
 C:Keywords: aminoacyltransferase; calcium binding
 F:268/Active site: Cys #status predicted

Query Match 9.8%; Score 71; DB 2; Length 684;
 Best Local Similarity 21.8%; Pred. No. 34;
 Matches 22; Conservative 16; Mismatches 39; Indels 24; Gaps 2;

QY 23 TPTCYSRMRALSOEITRDFNLLQVSESPFCVRLPRVLDIHNVCVLDKLRDFVASPP 82
 DB 82 TPDHYNQWATLQNESKGVTVATSSFNAILGKI--QLNVKYNHI----- 126

QY 83 CWKVAQVDSLKKARKLYTIMNSFCRRDLVFLDLDCCNALEY 123
 DB 127 -----LJSEENILYLLFPNCKEDWFMPEDESKKEY 158

RESULT 10
 Q00WC2
 B256 protein - cassava latent virus (West Kenyan isolate 844)
 C:Species: cassava latent virus
 C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
 C:Accession: A04168
 R:Stanley, J.; Gay, M.R.
 Nature 301, 260-262, 1983
 A:Title: Nucleotide sequence of cassava latent virus DNA.
 A:Reference number: A04164
 A:Accession: A04168
 A:Molecule type: DNA
 A:Residues: 1-256 <STA>
 C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A an
 C:Genetics:
 A:Map position: segment B
 C:Superfamily: tomato golden mosaic virus BR1 protein

Query Match 9.7%; Score 70; DB 1; Length 256;
 Best Local Similarity 30.3%; Pred. No. 14;
 Matches 27; Conservative 14; Mismatches 30; Indels 18; Gaps 3;

QY 42 FNLLQVSESPFCVRLPR-----YLDI-----HNYCVLDKLRDFVASPPC 83
 DB 128 FSLIMDKPYLPAGVQGLPTEELFGPVACVYNLRLNLLNQHQHRYVRLHVSVKRFVSSSG 187

QY 84 WKVAQVDSLKKARKLYTIMNSFCRRDLV 112
 DB 188 TKVSQFRENKRLSTRRYTIWAFHGDGLV 216

RESULT 11
 S71512
 glucuronosyltransferase (EC 2.4.1.17) - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999
 C:Accession: S17512
 R:Wootter, R.; Sutherland, L.; Ebner, T.; Clarke, D.; da Cruz e Silva, O.; Burchell, B.
 Biochem. J. 278, 465-469, 1991
 A:Title: Cloning and stable expression of a new member of the human liver phenol/biliru
 A:Reference number: S17512; MUID:91378895; PMID:1910331
 A:Accession: S17512
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-530 <WOO>
 A:Cross-references: GB:S55985; NID:g233453; PIDN:AAH19791.1; PID:g233454
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 9.7%; Score 70; DB 2; Length 530;
 Best Local Similarity 28.8%; Pred. No. 32;
 Matches 44; Conservative 21; Mismatches 50; Indels 38; Gaps 10;

QY 3 TPGLPLVLLLLAG-APAAAR----PTPTCYSRMRALSOE-ITRDFNLLQVSESPFCVR 56
 DB 8 SPLPLCVLLLTCTGFAEAGKLVVPMGDSHMTMRSVVEKLILRGHVVVVSARGELATG 67

QY 57 YLPRLYL-DIHNVCVLDKLRDFVA-SPPCWKVAQVDSL----- 92
 DB 68 KINELHSEDLFNFIYLEDLDFEFKFAHAQWK-AQVRYSIYLLMGSYNDIFDLFFSNCRS 126

QY 93 --KDARKLYTIMNSFCRRDLVFL--LDDCNAL 121
 DB 127 LFKDKKLYLKESSP---DAVFLDFDNGGLI 156

RESULT 12
 AF0611
 cell division protein FtsK [imported] - Salmonella enterica subsp. enterica serovar Tyf
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AF0611
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
 , S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AF0611
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1343 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05360.1; PID:g16502124; GSPDB:GN00176
 C:Genetics:
 A:Gene: STV0958

Query Match 9.7%; Score 70; DB 2; Length 1343;
 Best Local Similarity 24.5%; Pred. No. 94;

Matches 37; Conservative 15; Mismatches 61; Indels 38; Gaps 5;
 2 RTGPGPLVLLILLAGAPAAARTPTTCYGRMRALSQEIITRDNLLQVSESEPCVRYLPRL 61
 849 RPTPLPSLDLLTPPSEVEPVDITPALQMARLVEARLADF-----RI 891
 62 YLDIHNYCVLDKLRDFVAS--PPCKVAQVDSL--KDKARKLYTIMNSFC-----107
 892 KADVNYSGPVTITRFELNAPGVKAARISNLSRDLARSLSTVAVRVVEVIPGKPYVGLE 951
 108 ----RRDLVEL---LDDCNALREYRIPVTIVL 131
 952 LPNKKRQTVILREVLDNAKFRNPSPLTIVL 982

RESULT 13
 S76762
 hypothetical protein slr0655 - Synecocystis sp. (strain PCC 6803)
 C:Species: Synecocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S76762
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O.K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
 s.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76762
 A:Status: nucleic acid sequence not shown; translation not shown.
 A:Molecule type: DNA
 A:Residues: 1-180 <KAN>
 A:Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAAL8674.1; PID:dl01940
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 9.6%; Score 69.5; DB 2; Length 180;
 Best Local Similarity 34.5%; Pred. No. 10;
 Matches 30; Conservative 5; Mismatches 19; Indels 33; Gaps 6;
 22 PTPPTCYGRMRALSQEIITRDNLLQVSESEPCVRYLPRL-----YLDI-- 65
 18 PRPP-----RVEASSQVVVVCBGITADSLQTVLETSHPVYFFPRQDVETELDIST 73
 66 -HNYC-----VLDKLRDFA 79
 74 RHYCEWKGEAGYHFLSGDRDRDVA 100

RESULT 14
 S35515
 site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) - Bacillus subtilis
 N:Alternate names: modification methyltransferase BsuBI; site-specific DNA-methyltransferase
 C:Species: Bacillus subtilis
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
 C:Accession: S35515; S36924
 R:Xu, G.L.; Kapfer, W.; Walter, J.; Trautner, T.A.
 Nucleic Acids Res. 20, 6517-6523, 1992
 A:Title: BsuBI-an isospecific restriction and modification system of PstI: characterization
 A:Reference number: S35515; MUID:93126092; PMID:1480472
 A:Accession: S35515
 A:Molecule type: DNA
 A:Residues: 1-501 <XUG>
 A:Cross-references: EMBL:L01541
 A:Experimental source: strain ISB8
 A:Note: part of this sequence was confirmed by protein sequencing
 R:Birkenbihl, R.P.; Subramani, S.
 submitted to the EMBL Data Library, September 1992
 A:Reference number: S36924
 A:Accession: S36924
 A:Molecule type: DNA
 A:Residues: 1-495, 'N', 497-501 <BIR>
 A:Cross-references: EMBL:L01541; NID:g143053; PIDN:AAA18169.1; PID:g143054
 C:Comment: This site-specific methylase recognizes the double-stranded hexanucleotide 5'

e BsuBI (or PstI) endonuclease (see PIR:S35516).
 C:Superfamily: site-specific DNA-methyltransferase (adenine-specific) PstI
 C:Keywords: methyltransferase; restriction modification system; S-adenosylmethionine

Query Match 9.5%; Score 69; DB 1; Length 501;
 Best Local Similarity 28.0%; Pred. No. 38;
 Matches 23; Conservative 19; Mismatches 24; Indels 16; Gaps 5;
 32 RALSOEITR--DFNLLQVSESEPCVRYLPRL-----YLDIHNYCVLDKLRDFVASPPCW 84
 69 RLISENIGKADLHLEIDEMLP---YLSEPLALFKDYIEINSQIIIDDFIEWAA-----Y 121
 85 KVAQVDSL--KDKARKLYTIMN 104
 122 SLDEESLLAKDKORFTHAILN 143

RESULT 15
 S33028
 hypothetical protein - human herpesvirus 4
 C:Species: human herpesvirus 4, Epstein-Barr virus
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
 C:Accession: S33028
 R:Farrell, P.J.
 submitted to the EMBL Data Library, March 1988
 A:Reference number: S32973
 A:Accession: S33028
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-201 <FAR>
 A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24823.1; PID:e25025; PID:g1334887

Query Match 9.4%; Score 68.5; DB 2; Length 201;
 Best Local Similarity 28.1%; Pred. No. 15;
 Matches 36; Conservative 14; Mismatches 45; Indels 33; Gaps 8;
 14 LAGAPAAARTPTTCYGRMRALSQEIITRDNLLQVSESEPCVRY--LPR-----L 61
 77 LAARPEADKAPPS--HDHLLTLVRDLTRRL-----APGRRNRFWALPRAMQLRRLRAGL 129
 62 YLDIHNYCVLDKLRDFVASPPCKVAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNAL 121
 130 RLSGSHVCLLDK--DGAAPAC--QTATHEGLSPTA-----YFREIMAFLLDVISAL 177
 122 E--YPIPV 127
 178 HPGYTIPTM 185

Search completed: February 25, 2004, 05:03:21
 Job time : 23 secs

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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:00:01 ; Search time 18 Seconds
(without alignments)
396.312 Million cell updates/sec

Title: US-10-023-282-310
Perfect score: 725
Sequence: 1 MRTGPLEPVLLLLAGAPAA.....CNALEYPIPTVTLVLPDRQRX 137

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	724	99.9	136	1	C17_HUMAN	Q9nr11 homo sapien
2	79.5	11.0	592	1	FZD1_CHICK	O57328 gallus gall
3	76	10.5	838	1	YKAA_CAEEL	P34261 caenorhabdi
4	75	10.3	114	1	SZ06_HUMAN	P80162 homo sapien
5	75	10.3	615	1	FA12_HUMAN	P00748 homo sapien
6	73.5	10.1	846	1	SBP2_RAT	Q9gx72 rattus norv
7	71.5	9.9	188	1	RNFE_PSEAE	Q9hyb9 pseudomonas
8	71.5	9.9	684	1	SGT1_DROME	Q9w032 drosophila
9	71.5	9.9	781	1	TL22_CHICK	Q9d936 gallus gall
10	71.5	9.9	793	1	IL3R_HUMAN	Q9dd78 gallus gall
11	71	9.8	378	1	IL3R_HUMAN	P26951 homo sapien
12	71	9.8	684	1	TGM4_HUMAN	P49221 homo sapien
13	71	9.8	854	1	SBP2_HUMAN	Q96t21 homo sapien
14	70.5	9.7	236	1	ISPD_EUCAP	Q8k9d6 buchnera ap
15	70	9.7	256	1	VBRI_CLVCK	P03565 cassava lat
16	70	9.7	530	1	UD12_HUMAN	P36509 homo sapien
17	70	9.7	883	1	HSS2_HUMAN	P52849 homo sapien
18	70	9.7	1343	1	FTSK_SALTI	Q8z814 salmonella
19	70	9.7	1351	1	FTSK_SALTY	Q8z8d5 salmonella
20	69	9.5	501	1	MTBE_BACSU	P33563 bacillus su
21	68	9.4	256	1	VBRI_CLVCK	P14970 cassava lat
22	68	9.4	342	1	LUM_BOVIN	Q05443 bos taurus
23	68	9.4	382	1	EDG1_MOUSE	O08530 mus musculu
24	68	9.4	383	1	EDG1_RAT	P48303 rattus norv
25	68	9.4	469	1	YOJ8_CAEEL	P34631 caenorhabdi
26	67.5	9.3	534	1	RYK_MOUSE	Q01887 mus musculu
27	67.5	9.3	876	1	VP41_CAEEL	Q19954 caenorhabdi
28	67	9.2	219	1	V441_VACCC	P21064 vaccinia vi
29	67	9.2	219	1	V441_VACCV	P24766 vaccinia vi
30	67	9.2	372	1	GDF1_HUMAN	P27539 homo sapien
31	67	9.2	522	1	TSAW_RICTS	P37919 rickettsia
32	67	9.2	593	1	FA12_BOVIN	P98140 bos taurus
33	67	9.2	687	1	SSY5_YEAST	P47002 saccharomyc

RESULT 1
C17_HUMAN
ID C17_HUMAN STANDARD; PRT; 136 AA.
AC Q9NR11;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytokine-like protein C17 precursor.
GN C4ORF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RC TISSUE=Blood;
RX MEDLINE=20313895; PubMed=10857752;
RA Liu X., Rapp N., Deans R., Cheng L.;
RT "Molecular cloning and chromosomal mapping of a candidate cytokine
RT gene selectively expressed in human CD34+ cells.";
RL Genomics 65:283-292(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Specifically expressed in CD34+ hematopoietic
CC cells.
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34 66.5 9.2 901 1 VP3_BT2A
35 66 9.1 212 1 GIDB_XYLFA
36 66 9.1 212 1 GIDB_XYLFT
37 66 9.1 381 1 EDG1_HUMAN
38 66 9.1 454 1 Y1D4_MYCTU
39 66 9.1 488 1 RN23_MOUSE
40 66 9.1 784 1 TLR2_CRIGR
41 66 9.1 1329 1 FTSK_ECOLI
42 66 9.1 1342 1 FTSK_ECO57
43 66 9.1 1342 1 FTSK_SHIFL
44 66 9.1 1347 1 FTSK_ECOL6
45 66 9.1 1403 1 VG22_HSVI1

ALIGNMENTS

CC EMBL; AF193766; AAF33372.1; -
CC EMBL; BC031391; AAH31391.1; -
CC MM; 607930; -
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0005625; S:soluble fraction; TAS.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
KW Signal.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 136 CYTOKINE-LIKE PROTEIN C17.
SQ SEQUENCE 136 AA; 1557 MW; 1CAE1BFC3IA3A33 CRC64;

Query Match 99.9%; Score 724; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.2e-66;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTPGPPVLLVLLAGAPAPPTPTCYSMRALSQETTRDFNLLQVSESEPCVRLPR 60
DB 1 MRTPGPPVLLVLLAGAPAPPTPTCYSMRALSQETTRDFNLLQVSESEPCVRLPR 60

QY 61 LYLDIHCYVLDKLRDFVAPPCWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120
DB 61 LYLDIHCYVLDKLRDFVAPPCWKAQVDSLKDKARKLYTIMNSFCRDLVFLDDCNA 120

QY 121 LEYPIPTVTLPRQR 136
DB 121 LEYPIPTVTLPRQR 136

RESULT 2
FZD1_CHICK STANDARD; PRT; 592 AA.
AC OS7328; Q9IA07;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Frizzled 1 precursor (Frizzled-1) (Fz-1) (cfZ-1).
GN FZD1 OR FZ1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb bud;
RX MEDLINE=98260739; PubMed=9598377;
RA Kengaku M., Twombly V., Tabin C.;
RT "Expression of Wnt and Frizzled genes during chick limb bud development";
RL Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).
RN [2]
RP SEQUENCE OF 307-592 FROM N.A.
RX MEDLINE=20245319; PubMed=10781956;
RA Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.;
RT "Characterization of avian frizzled genes in cranial placode development";
RL Mech. Dev. 93:195-200(2000).
CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed in the lens, otic placode (medial wall of the vesicle) and in epibranchial placode. Also expressed in the developing somites (dermomyotome).
CC -!- DEVELOPMENTAL STAGE: Somites and placodal expression appears at stage 9. At this stage, more obvious expression is detected in the neural tube (midbrain and rostral hindbrain), and persists through about stage 15. Strongly expressed in the ectoderm and around the otic placodes at stage 12. At stage 16, otic expression declines, expression in epibranchial placodes begins and peaks at stage 20. Expression in the lens of the eye is first seen at about stage 15, more evident at stage 16. At stage 17, seen in the ectoderm and mesenchyme of the limb primordia. Detected at stage 20 in the lip of the optic cup, in the mesenchyme surrounding the eye, in the ectoderm overlying the lens and in the ectoderm caudal and ventral of the olfactory placodes. From stages 20-30, expressed in cartilage and in the dermomyotomes and migrating sclerotomal cells forming vertebrae.
CC -!- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).
CC -!- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By similarity).
CC -!- SIMILARITY: Belongs to the Fz/Smo G-protein coupled receptor family.
CC -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
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CC EMBL; AF031830; AAB87968.1; -
CC EMBL; AF224314; AAF61094.1; -
CC InterPro; IPR000539; Frizzled.
CC InterPro; IPR000024; Fz domain.
CC Pfam; PF01534; Frizzled; 1.
CC Pfam; PF01392; Fz; 1.
CC PRINTS; PR00489; FRIZZLED.
CC SMART; SM00603; FRI; 1.
CC PROSITE; PS50038; FZ; 1.
CC PROSITE; PS50261; G PROTEIN RECEPTOR; Transmembrane;
CC Multigene family; G-protein coupled receptor; Glycoprotein; Signal.
CC Developmental protein; Wnt signaling pathway; Signal.
CC SIGNAL 1 48
FT CHAIN 49 592
FT DOMAIN 271 271 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 272 292 1 (POTENTIAL).
FT DOMAIN 293 303 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 304 324 2 (POTENTIAL).
FT DOMAIN 325 351 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 352 372 3 (POTENTIAL).
FT DOMAIN 373 394 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 395 415 4 (POTENTIAL).
FT DOMAIN 416 438 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 439 459 5 (POTENTIAL).
FT DOMAIN 460 485 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 486 506 6 (POTENTIAL).
FT DOMAIN 507 527 7 (POTENTIAL).
FT TRANSMEM 528 552 8 (POTENTIAL).
FT DOMAIN 553 584 9 (POTENTIAL).
FT SITE 570 575 LYS-THR-X-X-X-TRP MOTIF.
FT SITE 590 592 PDZ-BINDING.
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 592 AA; 65490 MW; 933E76063CA6109D CRC64;

Query Match 11.0%; Score 79.5; DB 1; Length 592;
Best Local Similarity 23.3%; Pred. No. 2.2;

Matches 37; Conservative 16; Mismatches 45; Indels 61; Gaps 7;
QY 2 RFPGLPVLILLIA-----GAPAAPPTPTCYSRMALSQBITRDNLLQVSEPCV 55
DB 28 RPPALPVLILLIAALPAGGQPAQA-----ALSER-----GISIPD----- 66
QY 56 RYLPRIYLDHNVCLDKRDFVSPPCWVKVQVDSLKD-----KARKLYTI 102
DB 67 -----HGYC-----QPISTPLCTDIAYNQTIMPLNGLHTNQEDAGLEVHQFYPL 110
QY 103 MNSFCRDIIVFLDD-----CNALEYPIPVTVTLPRQR 136
DB 111 VKVQCSAEKFFELGMYAPVCTVLEQALPPCRSLCERAR 149
RESULT 3
YKAA CAEEL STANDARD; PRT; 838 AA.
AC P34261; P34262;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Hypothetical protein B0303.11 in chromosome III.
GN B0303.11/B0303.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=92168156; PubMed=1538779;
RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
RA Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear S., Coulson A.,
RA Craxton M., Durbin R., Berks M., Metzstein M., Hawkins T.,
RA Ainscough R., Waterston R.;
RT "The C. elegans genome sequencing project: a beginning."
RN Nature 356:37-41(1992).
RP REVISIONS.
RA Waterston R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M77697; AAA27902.3; --
DR PIR; S27792; S27792.
DR WormPep; B0303.11; CE29539.
KW Hypothetical protein.
SQ SEQUENCE 838 AA; 93432 MW; AD0C015A7C760646 CRC64;
Query Match 10.5%; Score 76; DB 1; Length 838;
Best Local Similarity 33.74; Fred. No. 7.4;
Matches 28; Conservative 15; Mismatches 28; Indels 12; Gaps 4;
QY 11 LLLAGAPAAPPTPTCYSRMALSQBITRDNLLQVSE--PGEPCVR-YLPRIYLD--I 65
DB 412 ILLSGSPARP-----GLVDFAHSHITRKSLLICGYIIPQSPCSRYLLQLKDKQI 464
QY 66 HNYCVLDKLRDFVSPPCWVKVQVDSLKD-----KARKLYTI 102
DB 465 NDWLRAREVNAFGAICCTKQAE 487
RESULT 4
SZ06 HUMAN STANDARD; PRT; 114 AA.
ID -SZ06_HUMAN

AC P80162;
DT 01-APR-1993 (Rel. 25, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine B6 precursor (CXCL6) (Granulocyte chemotactic
DE protein 2) (GCP-2) (Chemokine alpha 3) (CKA-3).
GN CXCL6 OR SCYB6 OR GCP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC ROVAI L.E., HERSCHMAN H.R., SMITH J.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA NI J., SU J., LI H.;
RT "Cloning, sequencing and biological characterization of a C-X-C
RT chemokine, CKA-3."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA STRAUSBERG R.L., FEINGOLD E.A., GROUSE L.H., DERGE J.G.,
RA KLAUNER R.D., COLLINS F.S., WAGNER L., SHENMEN C.M., SCHULER G.D.,
RA ALTACHUL S.P., ZEEBERG B., BUETOW K.H., SCHAEFER C.F., BHAT N.K.,
RA HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F.,
RA DIATCHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L.,
RA STAPLETON M., SOARES M.B., DONALDO M.F., CASAVANT I.L., SCHEETZ T.E.,
RA BROWNSTEIN M.J., USDIN T.B., TOSHIYUKI S., CARMINCI P., PRANGE C.,
RA RAHA S.S., LOQUELLANO N.A., PETERS G.J., ABRAMSON R.D., MULLAHY S.J.,
RA BOSAK S.A., MCBWAN P.J., MCKERNAN K.J., MALEK J.A., GUNARATNE P.H.,
RA RICHARDS S., WORLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W.,
RA VILLALON D.K., MUZNY D.M., SODERGREN E.J., LU X., GIBBS R.A.,
RA FAHEY J., HELTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A.,
RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BOUFFARD G.G.,
RA BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C.,
RA RODRIGUEZ A.C., GRIMWOOD J., SCHMUTZ J., MYERS R.M.,
RA BUTTERFIELD Y.S.N., KRZYWINSKI M.I., SKALEKA U., SMAILL D.E.,
RA SCHNERCH A., SCHEIN J.E., JONES S.J.M., MARRA M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 38-114 FROM N.A.
RX MEDLINE=97210779; PubMed=9057843;
RA FROYEN G., PROOST P., RONSE I., MITERA T., HAELENS A., WUYTS A.,
RA OPDENAKKER G., VAN DAMME J., BILLIAU A.;
RT "Cloning, bacterial expression and biological characterization of
RT recombinant human granulocyte chemotactic protein-2 and differential
RT expression of granulocyte chemotactic protein-2 and epithelial cell-
RT derived neutrophil activating peptide-78 mRNAs."
RL Eur. J. Biochem. 243:762-769(1997).
RN [5]
RP SEQUENCE OF 38-112.
RC TISSUE=Osteosarcoma;
RX MEDLINE=94001982; PubMed=8399143;
RA PROOST P., WUYTS A., CONINGS R., LENAERTS J.-P., BILLIAU A.,
RA OPDENAKKER G., VAN DAMME J.;
RT "Human and bovine granulocyte chemotactic protein-2: complete amino
RT acid sequence and functional characterization as chemokines."
RL Biochemistry 32:10170-10177(1993).
RN [6]
RP SEQUENCE OF 38-57.
RC TISSUE=Osteosarcoma;
RX MEDLINE=93139489; PubMed=8423327;
RA PROOST P., DE WOLF-PEETERS C., CONINGS R., OPDENAKKER G., BILLIAU A.,
RA VAN DAMME J.;
RT "Identification of a novel granulocyte chemotactic protein (GCP-2)
RT from human tumor cells. In vitro and in vivo comparison with natural
RT forms of GRO, IP-10, and IL-8."

RL J. Immunol. 150:1000-1010(1993).
CC -!- FUNCTION: Chemotactic for neutrophil granulocytes.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokine Cx) family.
CC
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U83303; AAC51338.1; -;
CC EMBL; U81234; RAD00506.1; -;
CC EMBL; BC013744; AAH13744.1; -;
CC EMBL; Y08770; CAA70023.1; -;
CC HSP; P10889; IWI2.
CC Genew; HGNC:10643; CXCL6.
CC MIM; 138965; -;
CC GO; GO:0008009; P:chemokine activity; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR00437; SMALLCYTKCX.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
CC Cytokine; Chemotaxis; Heparin-binding; Signal.
KW SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 114 SMALL INDUCIBLE CYTOKINE B6.
FT CHAIN 40 114 SMALL INDUCIBLE CYTOKINE B6, N-PROCESSED
FT CHAIN 43 114 SMALL INDUCIBLE CYTOKINE B6, N-PROCESSED
FT CHAIN 46 114 SMALL INDUCIBLE CYTOKINE B6, N-PROCESSED
FT CHAIN 49 75 BY SIMILARITY.
FT DISULFID 51 91 BY SIMILARITY.
FT SEQUENCE 114 AA; 11897 MW; 5A58B38C17F25178 CRC64;
SQ
Query Match 10.3%; Score 75; DB 1; Length 114;
Best Local Similarity 29.0%; Pred. No. 0.95;
Matches 36; Conservative 13; Mismatches 47; Indels 28; Gaps 4;
QY 2 RTPGP-----LPVLLLLAGAPAAARPTPTCYSRMRALSOEITRDFNLLQVSEPEPCV 55
Db 10 RVPGSGSLCALLALLLL-----TPPGPLASAGPVAVLT-----ELRCTCL 52
QY 56 RYLPLRYLDHNYCYVLDKLRDFVAPPCWQVADSLKDKARKLYTIMNSFCRRDLVFL 115
Db 53 RVTLRV-----NPKTIGKLVPPAGPQCSKEVWASLNGKQVCLDPEAPFLKVIQKIL 107
QY 116 DDCN 119
Db 108 DSGN 111
RESULT 5
FA12 HUMAN
ID FA12 HUMAN STANDARD; PRT; 615 AA.
AC P00748; P78339;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
DE (HAF).
GN F12.
OS Homo sapiens (Human).

OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN RN NCBI_TaxID=9606;
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=88007593; PubMed=2888762;
RA RA Cool D.E., McGillivray R.T.A.;
RT RT "Characterization of the human blood coagulation factor XII gene.
RT Intron/exon gene organization and analysis of the 5'-flanking
RT region.";
RL J. Biol. Chem. 262:13662-13673(1987).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605.
RA Rieder M.J., Amel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 4-615 FROM N.A.
RX RX MEDLINE=86176794; PubMed=3754331;
RA Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,
RA Cortese R.;
RT "cDNA sequence coding for human coagulation factor XII (Hageman).";
RL Nucleic Acids Res. 14:3146-3146(1986).
RN [4]
RP SEQUENCE OF 14-615 FROM N.A.
RX RX MEDLINE=86033830; PubMed=3877053;
RA Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D.,
RA McGillivray R.T.A.;
RT "Characterization of human blood coagulation factor XII cDNA.
RT Prediction of the primary structure of factor XII and the tertiary
RT structure of beta-factor XIIa.";
RL J. Biol. Chem. 260:13666-13676(1985).
RN [5]
RP SEQUENCE OF 146-615 FROM N.A.
RX RX MEDLINE=86216049; PubMed=3011063;
RA Que B.G., Davie E.W.;
RT "Characterization of a cDNA coding for human factor XII (Hageman
RT factor).";
RL Biochemistry 25:1525-1528(1986).
RN [6]
RP SEQUENCE OF 20-379.
RX RX MEDLINE=85182674; PubMed=3886654;
RA McMullen B.A., Fujikawa K.;
RT "Amino acid sequence of the heavy chain of human alpha-factor XIIa
RT (activated Hageman factor).";
RL J. Biol. Chem. 260:5328-5341(1985).
RN [7]
RP SEQUENCE OF 354-362 AND 373-615.
RX RX MEDLINE=83291041; PubMed=6604055;
RA Fujikawa K., McMullen B.A.;
RT "Amino acid sequence of human beta-factor XIIa.";
RL J. Biol. Chem. 258:10924-10933(1983).
RN [8]
RP SEQUENCE OF 561-615 FROM N.A.
RC RC TISSUE=Blood;
RX RX MEDLINE=96133302; PubMed=8528215;
RA Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Engel W.;
RT "The novel acceptor splice site mutation 11396(G-->A) in the factor
RT XII gene causes a truncated transcript in cross-reacting material
RT negative patients.";
RL Hum. Mol. Genet. 4:1235-1237(1995).
RN [9]
RP CARBOHYDRATE-LINKAGE SITE THR-109.
RX RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107(1992).
RN [10]
RP VARIANT WASHINGTON D.C. SER-590.
RX RX MEDLINE=90046788; PubMed=2510163;
RA Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B.,
RA Saito H.;

"Coagulation factor XII (Hageman factor) Washington D.C.: inactive factor Xlla results from Cys-571-->Ser substitution.";
Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322 (1989).
[11]
VARIANT LOCARNO PRO-372.
MEDLINE=94325559; PubMed=8049433;
RA Hovington J.K., Schaller J., Stricker H., Wuillemin W.A., Furlan M., Laemmle B.;
RT "Coagulation factor XII Locarno: the functional defect is caused by the amino acid substitution Arg-353-->Pro leading to loss of a kallikrein cleavage site.";
Blood 84:1173-1181 (1994).
[12]
VARIANT TENRI CYS-53.
MEDLINE=99290785; PubMed=10361128;
RA Kondo S., Tokunaga F., Kawano S., Oono Y., Kumagai S., Koide T.;
RT "Factor XII Tenri, a novel cross-reacting material negative factor XII deficiency, occurs through a protease-mediated degradation.";
Blood 93:4300-4308 (1999).
CC -!- FUNCTION: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.
CC -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor VII to form factor VIIa and factor XI to form factor Xla.
CC -!- PTM: O- AND N-GLYCOSYLATED.
CC -!- DISEASE: Defects in F12 do not cause any clinical symptoms. The sole effect is that whole-blood clotting time is prolonged.
CC -!- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a complex bound to an anionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor Xlla and then to beta-factor Xlla. Alpha-factor Xlla activates factor XI to factor Xla.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
CC -!- SIMILARITY: Contains 1 fibronectin type II domain.
CC -!- SIMILARITY: Contains 1 kringle domain.

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EMBL; M31315; AAA70225.1; -;
DR EMBL; AF538691; RAM97932.1; -;
DR EMBL; M11723; AAA51986.1; -;
DR EMBL; M17466; AAB59490.1; -;
DR EMBL; M17464; AAB59490.1; JOINED.
DR EMBL; M17465; AAB59490.1; JOINED.
DR EMBL; M13147; AAA70224.1; -;
DR EMBL; U71274; AAB51203.1; -;
DR PIR; A29411; KFHU12.
DR HSP; P00763; IDPO.
DR MEROPS; S01.211; -;
DR Genew; HGNC:3530; F12.
MIM; 234000; -;
DR GO; GO:0003805; F:blood coagulation factor XI activity; TAS.
DR GO; GO:0003806; F:blood coagulation factor XII activity; TAS.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR GO; GO:0007596; F:blood coagulation; TAS.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibnctnl.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00039; fn1; 1.

DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00013; ENTPPEII.
DR PRINTS; PR00018; KRINGHE.
DR ProDom; PD000995; FN_Type_II; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
KW Hydrolase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen;
KW Polymorphism; Disease mutation.
FT SIGNAL 1 19
FT CHAIN 20 372 ALPHA-FACTOR XIIA HEAVY CHAIN.
FT CHAIN 373 615 ALPHA-FACTOR XIIA LIGHT CHAIN.
FT CHAIN 354 362 BETA-FACTOR XIIA PART 1.
FT CHAIN 373 615 BETA-FACTOR XIIA PART 2.
FT DOMAIN 47 88 FIBRONECTIN TYPE-II.
FT DOMAIN 94 131 EGF-LIKE 1.
FT DOMAIN 133 173 FIBRONECTIN TYPE-I.
FT DOMAIN 174 210 EGF-LIKE 2.
FT DOMAIN 217 295 KRINGLE.
FT DOMAIN 296 349 PRO-RICH.
FT DOMAIN 373 615 SERINE PROTEASE.
FT CARBOHYD 109 109 O-LINKED (FUC).
FT CARBOHYD 249 249 N-LINKED (GLCNAC...).
FT CARBOHYD 299 299 O-LINKED (POTENTIAL).
FT CARBOHYD 305 305 O-LINKED (POTENTIAL).
FT CARBOHYD 308 308 O-LINKED (POTENTIAL).
FT CARBOHYD 328 328 O-LINKED (POTENTIAL).
FT CARBOHYD 329 329 O-LINKED (POTENTIAL).
Query Match 10.3%; Score 75; DB 1; Length 615;
Best Local Similarity 25.5%; Pred No. 6.5;
Matches 26; Conservative 12; Mismatches 36; Indels 28; Gaps 5;
QY 2 RTPGELPVLLLLAGAPAAARTPP-----TCYSRNRALSQEITRDNLLQVSESEP 53
336 QTPGAL-----PAKREQPPSLTRNGPLSCQQLRKLSSMTRVVGGLVALRGAHP 385
Db 54 CVRIPLRIYLDIHNYCVKLDKDRFVASPPCKWQVQVDSLKDK 95
386 ---XIALYWG-HSFCAGSLI-----APCWVLTAAHCLQDR 417
RESULT 6
SBP2_RAT
ID SBP2_RAT STANDARD; PRT; 846 AA.
AC Q9QX72;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE SECIS-binding protein 2.
GN SBP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

SEQUENCE FROM N.A.
TISSUE=Testis; PubMed=10637234;
MEDLINE=20105285; PubMed=10637234;
Copeland P.R., Fletcher J.E., Carlson B.A., Hatfield D.L.,
Driscoll D.M.;
"A novel RNA binding protein, SBP2, is required for the translation of
mammalian selenoprotein mRNAs";
EMBO J. 19:306-314(2000).
[2]
CHARACTERIZATION.
TISSUE=Testis;
MEDLINE=99395111; PubMed=10464275;
Copeland P.R., Driscoll D.M.;
"Purification, redox sensitivity, and RNA binding properties of SECIS-
binding protein 2, a protein involved in selenoprotein biosynthesis";
J. Biol. Chem. 274:25447-25454(1999).
- FUNCTION: Binds to the SECIS element in the 3'UTR of some mRNAs
encoding selenoproteins.
- SUBCELLULAR LOCATION: Nuclear (Potential).
- TISSUE SPECIFICITY: Ubiquitous.

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EMBL; AJ251245; CAB61692.1; -
InterPro; IPR004038; Ribosomal L7Ae.
Pfam; PF01248; Ribosomal L7Ae; 1.
Protein biosynthesis; RNA-binding; Nuclear protein.
DOMAIN 370 380 POLY-LYS.
DOMAIN 370 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DOMAIN 666 687 RNA-BINDING (POTENTIAL).
SEQUENCE 846 AA; 93299 MW; 416EDFDEA38A4A13 CRC64;

Query Match 10.18; Score 73.5; DB 1; Length 846;
Best Local Similarity 23.18; Pred. No. 13;
Matches 34; Conservative 23; Mismatches 45; Indels 45; Gaps 7;

QY 19 AARPTP-----PTCYSMRALSOEITDFNLLQVSEPEPC-----VRYLPRLY--- 62
Db 604 ACQAPDSATPKTHSR-----FRDYCSQMSKEVDACVTGLKELVRFQDRMTQKD 656
QY 63 -----LDIHNVCVLDKLRDFVAPSPCKVQVDSLKDKARKLYTMMNSFCR 108
Db 657 PVKAKTKRRLVLGLREVLKHLKRLKCIITSPNCEKTSQSGGLDD---TLHTIIDCACE 713

QY 109 RDL--VFLLDD---CNALEYPIPTTV 130
Db 714 QNIFVFALNRKALGRSLNKAVPSIV 740

RESULT 7
RNFb_PSEAE
ID -RNFb_PSEAE STANDARD; PRT; 188 AA.
AC Q9HYB9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Electron transport complex protein rnfB.
GN RNFb OR PA3490.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen";
Nature 406:959-964(2000).
- FUNCTION: May be part of a membrane complex involved in electron
transport (By similarity).
- COFACTOR: Binds 1 2Fe-2S and 2 4Fe-4S clusters (Potential).
- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC,
rnfD, rnfE and rnfG (By similarity).
- SUBCELLULAR LOCATION: Cytoplasmic; inner membrane-associated (By
similarity).
- SIMILARITY: Belongs to the 4Fe4S bacterial-type ferredoxin family.
RnfB subfamily.

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EMBL; AB004770; AAG06878.1; -
PIR; C83208; C83208.
HSSP; P00198; 1FCA.
HAMAP; MF_00463; 1.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR007202; FeS.
Pfam; PF00037; fe4; 2.
Pfam; PF04060; FeS; 1.
PROSITE; PS00198; 4Fe4S_FERREDOXIN; 2.
KW Electron transport; Metal-binding; Iron-sulfur; Iron; 2Fe-2S; 4Fe-4S;
KW Inner membrane; Complete proteome.
FT METAL 49 49 IRON-SULFUR 1 (2FE-2S) (POTENTIAL).
FT METAL 52 52 IRON-SULFUR 1 (2FE-2S) (POTENTIAL).
FT METAL 57 57 IRON-SULFUR 1 (2FE-2S) (POTENTIAL).
FT METAL 73 73 IRON-SULFUR 1 (2FE-2S) (POTENTIAL).
FT METAL 113 113 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 116 116 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 119 119 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 123 123 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
FT METAL 143 143 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
FT METAL 146 146 IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
FT METAL 149 149 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 153 153 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 188 AA; 20025 MW; FDC942CADC589B4 CRC64;

Query Match 9.94; Score 71.5; DB 1; Length 188;
Best Local Similarity 21.24; Pred. No. 3.8;
Matches 29; Conservative 22; Mismatches 59; Indels 27; Gaps 4;

QY 4 PGELPVLULLLAGAAPARPTPTCYSMRALSOEITDFNLLQVSEPEPCVYLPRLYL 63
Db 55 PGCKPYAEALAAAG-DKINKCPGGEATIRALDLDLEPEPLDABETPRVAYI----- 108
QY 64 DIHNYCVLDKLRDFVAPSPCKVQVDSLKDKARKLYTMMNSFCRDLVFLDDCNALEY 123
Db 109 -----REACIGCTGCKICQCPVDAIVGAARLMTVIADEC-----TGCDLCLE 151
QY 124 PIPVTY----LPDRQR 136
Db 152 PCPVDCIEMREIPDVR 168

RESULT 8
SGT1_DROME
ID -SGT1_DROME STANDARD; PRT; 684 AA.
AC Q9W032;
DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE SGT1 protein homolog CG5714.
 DE CG5714.
 GN Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Boutch J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkley; TISSUE=Head;
 RC MEDLINE=22426086; PubMed=12537559;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RA "A Drosophila full-length cDNA resource";
 RL Genome Biol. 3:RESEARCH080.1-RESEARCH080.8(2002).
 CC -1- SIMILARITY: BELONGS TO THE SGT1 FAMILY.
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 CC -----
 CC EMBL; AE003474; AAP47628.1; -;
 CC EMBL; AV051483; AAK29207.1; -;
 CC FlyBase; FBgn0035324; CG5714.
 DR DR
 DR EMBL; AE003474; AAP47628.1; -;
 DR EMBL; AV051483; AAK29207.1; -;
 DR FlyBase; FBgn0035324; CG5714.
 DR DR

SQ SEQUENCE 684 AA; 77907 MW; D59B5C943E352F30 CRC64;
 Query Match 9.9%; Score 71.5; DB 1; Length 684;
 Best Local Similarity 25.0%; Pred No. 17;
 Matches 37; Conservative 22; Mismatches 50; Indels 39; Gaps 9;
 QY 13 LLGAPAAPAP--TPPTCYSRMRALSQETTRDNLLQ---VSEPPSC-----VRYL 58
 Db 142 LLLEAADALPDWASPETCEQRVVLVGGHL-----QLQNSAASSQDKPLTMAMAVQIRWN 197
 QY 59 PRLY---LDIHNVCVLDKLDVFAVPPCKV-----AQVDSLKDKARKLYTIMNSF 106
 Db 198 PLYRCQSQEQS-CIDARLKEYQIAQPHFSIHQVLELPHLSAAQLLKQKPRLLSSAVRAP 256
 QY 107 CERDLVFLDDCNALV---YPIPVTVV 130
 Db 257 CERDSL---DIKALRTMEYFPPEATRV 280

RESULT 9
 TL22 CHICK
 ID TL22 CHICK STANDARD; PRT; 781 AA.
 AC Q9DGB6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Toll-like receptor 2 type 2 precursor.
 GN TLR2-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=21601652; PubMed=11590137;
 RA Fukui A., Inoue N., Matsumoto M., Nomura M., Yamada K., Matsuda Y.,
 RA Toyoshima K., Seva T.;
 RT "Molecular cloning and functional characterization of chicken Toll-
 RT like receptors. A single chicken Toll covers multiple molecular
 RT patterns.";
 RL J. Biol. Chem. 276:47143-47149(2001).
 CC -1- FUNCTION: Participates in the innate immune response to microbial
 CC agents. Acts via MyD88 and TRAF6, leading to NF-kappa-B
 CC activation, cytokine secretion and the inflammatory response.
 CC Mediates the response to mycoplasma macrophage-activating
 CC lipopeptide-2KD (MALP-2).
 CC -1- SUBUNIT: Binds MyD88 via their respective TIR domains. Binds TLR6
 CC via their respective extracellular domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in ovary. Also detected in
 CC brain, heart, lung, liver, spleen and kidney, and at low levels in
 CC gizzard, muscle, testis and proventriculus.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -1- SIMILARITY: Contains 13 leucine-rich (LRR) repeats.
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 CC -----
 CC EMBL; AB046533; BAB16842.1; -;
 CC HSSP; O60603; 1FYW.
 CC InterPro; IPR004075; IL1_receptor1.
 CC InterPro; IPR001611; LRR_
 CC InterPro; IPR000483; LRR_Cterm.
 CC InterPro; IPR003591; LRR_Type.
 DR DR
 DR EMBL; AB046533; BAB16842.1; -;
 DR HSSP; O60603; 1FYW.
 DR InterPro; IPR004075; IL1_receptor1.
 DR InterPro; IPR001611; LRR_
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Type.
 DR DR

FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 793 AA; 90766 MW; 2BF659D9305D4562 CRC64;
 Query Match 9.9%; Score 71.5; DB 1; Length 793;
 Best Local Similarity 25.0%; Pred. No. 20;
 Matches 28; Conservative 16; Mismatches 45; Indels 23; Gaps 6;
 QY 18 PAARPTPTCYSEMRALSOBTRDFNLLQVSESEPCVRYLPLXLDIHNVCVLDKLRDF 77
 Db 640 PKRAPTKDICYDAFVSSENDSNWNIMVQLEQAC-----PFRCLLKH-----RDF 688
 QY 78 VASPPCKVQAQ-VDSLKDKARKLYTIMNSF-----CRRDLVF-----LLDDCN 119
 Db 689 V--PGKWIVNDIIDSIEKSHKTLFVLSHFVQSEWCKYELDFSHFRLEDDENN 738
 RESULT 11
 IL3R_HUMAN STANDARD; PRT; 378 AA.
 AC P26951;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-3 receptor alpha chain precursor (IL-3R-alpha) (CD123 antigen).
 DE (IL3RAX OR IL3RA OR IL3RX) AND
 GN (IL3RAY OR IL3RA OR IL3RY)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92005668; PubMed=1833064;
 RA Kitamura T., Sato N., Arai K., Miyajima A.;
 RT "Expression cloning of the human IL-3 receptor cDNA reveals a shared
 RL beta subunit for the human IL-3 and GM-CSF receptors.";
 RL Cell 66:1165-1174(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: This is a receptor for interleukin 3.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain which is shared
 CC by the interleukin 3, interleukin 5, and GM-CSF receptors.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.

CC Subfamily 5.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; M74782; AA59148.1; --
 CC EMBL; BC035407; AAH35407.1; --
 CC FIR; A40266; A40266.
 CC Genew; HGNC:6012; IL3RA.
 CC MIM; 308385; --
 CC MIM; 430000; --
 CC GO; GO:0004912; F.interleukin-3 receptor activity; TAS.
 CC InterPro; IPR002996; CR1A.
 CC InterPro; IPR008957; FN III-like.
 CC InterPro; IPR003532; Hemopoietin S F2.
 CC PROSITE; PS01356; HEMATOPO. REC S F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 378 INTERLEUKIN-3 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 19 305 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 306 325 POTENTIAL.
 FT DOMAIN 326 378 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 45 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 378 AA; 43330 MW; 716CE1803F2E5FC0 CRC64;
 Query Match 9.8%; Score 71; DB 1; Length 378;
 Best Local Similarity 20.3%; Pred. No. 9.5;
 Matches 25; Conservative 13; Mismatches 37; Indels 48; Gaps 3;
 QY 10 LLLLLAGAPA-----ARPTPTCYSEMRALSOBTRDFNLLQVSESEPCVRYLPLXLD 64
 Db 6 LLLLLALPCLLTQTKEDFPPTITNLKAKAQLITWDLNR----- 45
 QY 65 IHNYCVLDKLRDFVASPPCKVQAQVDSLKDKARKLYTIMNSFCRRDLVFLDDPCNALEY 124
 Db 46 -----NVTIDECVKDADYSMPAVNNSYCFGAISL---CEVTNYT 82
 QY 125 IPV 127
 Db 83 VRV 85
 RESULT 12
 TGM4_HUMAN STANDARD; PRT; 684 AA.
 ID P49221; Q16707; Q96Q04;
 AC 01-FEB-1996 (Rel. 33, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-glutamine glutamyltransferase 4 (EC 2.3.2.13) (TGase 4)
 DE (Prostate transglutaminase) (TGP) (TG(P)) (Prostate-specific
 GN transglutaminase) (Fibrinoligase).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=94390018; PubMed=7916568;
 RA Grant F.J., Taylor D.A., Sheppard P.O., Mathewes S.L., Lint W.,
 RA Vanaja E., Bishop P.D., O'Hara P.J.;

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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:01:12 ; Search time 39 Seconds
(without alignments)

1108.359 Million cell updates/sec

Title: US-10-023-282-310

Perfect score: 725

Sequence: 1 MTPGGLPVLILLAGAPAA.....CNALEYPIPVTVLPDRQRX 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	12.1	557	13	O73658
2	85	11.7	277	16	Q7W159
3	85	11.7	277	16	Q7W690
4	82	11.3	1130	4	Q9C0D6
5	81.5	11.2	640	10	Q8L183
6	81	11.2	1141	10	Q9FLX0
7	80.5	11.1	264	16	Q7VXB5
8	77.5	10.7	1166	12	Q9QNC4
9	77.5	10.7	1670	12	Q1R167
10	75.5	10.4	1473	5	Q9VZY2
11	75	10.3	300	4	Q9GEF3
12	75	10.3	348	8	Q9TDS6
13	75	10.3	615	4	Q81Z25
14	75	10.3	1166	12	Q91E48
15	75	10.3	1670	12	Q91E49
16	75	10.3	1811	5	Q81L76

17	75	10.3	1901	12	Q9DHH8
18	74.5	10.3	174	4	Q8N7P0
19	74.5	10.3	174	11	Q8BJ96
20	74.5	10.3	174	11	Q8R143
21	74	10.2	343	16	Q9RZ24
22	74	10.2	390	4	Q9UEH7
23	74	10.2	430	4	Q8WK02
24	74	10.2	1895	12	Q9QAY3
25	73.5	10.1	571	5	Q861V2
26	73.5	10.1	662	10	Q7XUP1
27	73.5	10.1	1446	5	O97234
28	73	10.1	326	6	O8MK88
29	73	10.1	326	6	Q9BF60
30	73	10.1	327	10	Q8LHZ7
31	72.5	10.0	168	12	Q9JF72
32	72.5	10.0	223	12	Q8JL79
33	72.5	10.0	278	12	Q89194
34	72.5	10.0	279	12	Q88963
35	72.5	10.0	294	6	Q9MZV0
36	72.5	10.0	500	12	Q8OHU7
37	72.5	10.0	549	13	Q98UHS
38	72	9.9	240	6	Q9BF51
39	72	9.9	326	6	Q9BF48
40	72	9.9	326	6	Q9BF49
41	72	9.9	326	6	Q9BF47
42	72	9.9	326	6	Q9BF52
43	72	9.9	511	15	Q8JDT2
44	72	9.9	660	16	Q9WY25
45	71.5	9.9	422	10	Q7XQNS

ALIGNMENTS

RESULT 1

ID O73658 PRELIMINARY; PRT; 557 AA.
 AC O73658; 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE OIGSK-C.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98198545; PubMed=9539142;
 RA Hisatomi O., Matsuda S., Satoh T., Kotaka S., Imanishi Y.,
 RA Tokunaga F.;
 RT "A novel subtype of G-protein-coupled receptor kinase, GRK7, in
 RT teleost cone photoreceptors.";
 RL FEBS Lett. 424:159-164(1998).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. GPRK
 SUBFAMILY.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC EMBL; AB009568; EAA35670.1; -.
 DR HSP; P05132; IAPM.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004703; F:G-protein coupled receptor kinase activity; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000239; GPCR kinase.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR000342; Regl_Gprotein.
 DR InterPro; IPR002290; Ser_thr_kinase.


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DR InterPro: IP008271; Ser_thr_pkin_AS.
DR Pfam: PF0069; pkinase; 1.
DR Pfam: PF00615; RGS; 1.
DR PRINTS: PRO0717; GPCR_KINASE.
DR ProDom: PD000001; Prot_Kinase; 1.
DR SMART: SM00315; RGS; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00132; RGS; 1.
DR PROSITE: PS00132; RGS; 1.
KW ATP-binding: Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 557 AA; 63656 MW; A968753332E0065A CRC64;

Query Match
Best Local Similarity 12.1%; Score 88; DB 13; Length 557;
Matches 34; Conservative 13; Mismatches 22; Indels 40; Gaps 7;

QY 22 PTPPTCYSRMRALSOEITRDENLQVSEPCVRYLPRLYLDIHNVCVLDKLRDPVAVSP 81
DB 27 PTPPTCYSRMRALSOEITRDENLQVSEPCVRYLPRLYLDIHNVCVLDKLRDPVAVSP 81
QY 82 PCWKVAQ--VPSL-----KDKARKLYTIMNSFCRRD-----LVFL 114
DB 75 PEEKLAEEFLDYDWDLAEGRAKDKAQ--NIINKYKPSDKTFLTEL 121

RESULT 2
QY 7WI59 PRELIMINARY; PRT; 277 AA.
AC Q7WI59;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
GN BB2997.
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Larraga A.M., Temple L., James K., Basham D., Barris B., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Basham D., Cronin A., Davis P., Doggett J.,
RA Chillingworth T., Collins M., Cronin A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Squares S., Stevens K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 277 AA; 29829 MW; 6BDE0D447DB4F5A8 CRC64;

Query Match
Best Local Similarity 11.7%; Score 85; DB 16; Length 277;
Matches 46; Conservative 13; Mismatches 48; Indels 60; Gaps 8;

QY 1 MRPTEPPLP-----VLLLLLAGA-----PAARPTPTCYSRMRALSOEITR 40
DB 1 MRPTEPPLP-----VLLLLLAGA-----PAARPTPTCYSRMRALSOEITR 40
QY 41 DF-----NLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDPVAVSPCKVAVQ 89
DB 61 DFLRFCORNPCKPCLLAVSEPGDPS---LPBGLDI-----DIRTDVPRYVRWD 107

RESULT 4
QY 90 DSLKDK---ARKLYTIMNSFCRRDLVFLDDCN-----ALEYPIPV 127
DB 108 GKLVDPLDVRGLW-----RDDLVAFLLGCSFSEAMLENGLPV 147

Query Match
Best Local Similarity 11.7%; Score 85; DB 16; Length 277;
Matches 46; Conservative 13; Mismatches 48; Indels 60; Gaps 8;

QY 1 MRPTEPPLP-----VLLLLLAGA-----PAARPTPTCYSRMRALSOEITR 40
DB 1 MRPTEPPLP-----VLLLLLAGA-----PAARPTPTCYSRMRALSOEITR 40
QY 41 DF-----NLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDPVAVSPCKVAVQ 89
DB 61 DFLRFCORNPCKPCLLAVSEPGDPS---LPBGLDI-----DIRTDVPRYVRWD 107

RESULT 4
QY 90 DSLKDK---ARKLYTIMNSFCRRDLVFLDDCN-----ALEYPIPV 127
DB 108 GKLVDPLDVRGLW-----RDDLVAFLLGCSFSEAMLENGLPV 147

Query Match
Best Local Similarity 11.7%; Score 85; DB 16; Length 277;
Matches 46; Conservative 13; Mismatches 48; Indels 60; Gaps 8;

QY 1 MRPTEPPLP-----VLLLLLAGA-----PAARPTPTCYSRMRALSOEITR 40
DB 1 MRPTEPPLP-----VLLLLLAGA-----PAARPTPTCYSRMRALSOEITR 40
QY 41 DF-----NLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDPVAVSPCKVAVQ 89
DB 61 DFLRFCORNPCKPCLLAVSEPGDPS---LPBGLDI-----DIRTDVPRYVRWD 107

Query Match
Best Local Similarity 11.7%; Score 85; DB 16; Length 277;
Matches 46; Conservative 13; Mismatches 48; Indels 60; Gaps 8;

QY 1 MRPTEPPLP-----VLLLLLAGA-----PAARPTPTCYSRMRALSOEITR 40
DB 1 MRPTEPPLP-----VLLLLLAGA-----PAARPTPTCYSRMRALSOEITR 40
QY 41 DF-----NLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDPVAVSPCKVAVQ 89
DB 61 DFLRFCORNPCKPCLLAVSEPGDPS---LPBGLDI-----DIRTDVPRYVRWD 107

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RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIX.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:347-355(2000).
 DR EMBL; AB051514; BAB21818.1; -;
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR003104; FH2.
 DR Pfam; PF02181; FH2; 1.
 DR SMART; SM00498; FH2; 1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 1130 AA; 123263 MW; CC62F066CD2FE92F CRC64;

Query Match 11.3%; Score 82; DB 4; Length 1130;
 Best Local Similarity 27.5%; Pred. No. 4.6;
 Matches 25; Conservative 14; Mismatches 26; Indels 26; Gaps 5;

QY 28 YSRMRALSQBITRDFNLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDFVSPPCWKVA 87
 Db FVTKSLKENIQDGLCQME-----DFLOFAL-EKLRRL-----ECWK-- 406

QY 88 QVDSLKDKARKLYTINMSFCRRDLVFLDDC 118
 Db ---YTLIDFFCEDKTKMLDEC 432

RESULT 5
 Q8LI83 PRELIMINARY; PRT; 640 AA.
 AC Q8LI83;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ser/Thr protein kinase-like protein.
 GN OSJNB0093M23.4.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (CAS) genomic DNA, chromosome 1, BAC
 RT clone:OSJNB0093M23.4";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003854; BAC06279.1; -;
 DR Gramene; Q8LI83; -;
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001993; Mitoch carrier.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser thr pkinase.
 DR InterPro; IPR008271; Ser thr pkin_AS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00215; MITOCH CARRIER; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 640 AA; 67657 MW; DCB10EF4BCAAE121 CRC64;

Query Match 11.2%; Score 81.5; DB 10; Length 640;
 Best Local Similarity 28.4%; Pred. No. 2.8;
 Matches 48; Conservative 9; Mismatches 51; Indels 61; Gaps 8;

QY 4 PGPLPVLILL-----ACAPA-----ARPTPTCYSR----- 30
 Db PSLFLFLLLLLPPFAAVRSQAPAAPAQOCPPLNFTALRPFLAQLPFPDPSARCLLAVQS 65

QY 31 ---MRALSQBITRDFNLLQVSEPCVRYLPRLYLDIHNVCVLDKLRDFVSPPCWKVA 87
 Db VRLLLALHLAATGTFVLPANSSCLPPRAELP-FALPSPSACGLQGLDALLASPGC--A 121

QY 88 QVDSLKD-----KARKLYTINMSFCRRDLVFLDDCNALEYPIPVTT 129
 Db 122 NVSTLGDFAAVPSSR---ADNASCNRDLT-----PVPDCT 156

RESULT 6
 Q9FLX0 PRELIMINARY; PRT; 1141 AA.
 AC Q9FLX0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Genomic DNA, chromosome 5, P1 clone:MXC20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=98290546; PubMed=9628582;
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned p1 and TAC clones.";
 RL DNA Res. 5:41-54(1998).
 DR EMBL; AB009055; BAB10439.1; -;
 DR InterPro; IPR006906; Timeless.
 DR InterPro; IPR007725; TIMELESS_C.
 DR Pfam; PF04821; TIMELESS; 1.
 DR Pfam; PF05029; TIMELESS_C; 1.
 SQ SEQUENCE 1141 AA; 128902 MW; 334148C3A3D4252 CRC64;

Query Match 11.2%; Score 81; DB 10; Length 1141;
 Best Local Similarity 26.4%; Pred. No. 6;
 Matches 38; Conservative 23; Mismatches 59; Indels 24; Gaps 5;

QY 10 LLLLAGAPAAARPTPTCY-----SRMRALSQBITRDFNLL--QVSEPCVRYLPRL 61
 Db LLAHDVSPIQAGESTCYFLSRDQDFVLSRENVDIVITQTIEGNSLRHDLNLL 231

QY 62 YLDIHNVCVLDKLRDFVSP-----CWKVAQVDSLK-----DKARKLYTINMSFCRRDLV 112
 Db LLEIVHYVILLQGMELVAKAEKLDQKQASVDSLTKLMKEEVKRLARLNMMNRHSQ 291

QY 113 F-----LLDDCNALEYPIPVTT 129
 Db 232 FGGTFTRVTDGTRKAVLKGPSTT 315

RESULT 7
 Q7VXB5 PRELIMINARY; PRT; 264 AA.
 AC Q7VXB5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.

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GN BP1875.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
KW EMBL; BX640416; CAE42158.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 264 AA; 28281 MW; E4D4722DAFDDDB2A0 CRC64;

Query Match 11.1%; Score 80.5; DB 16; Length 264;
Best Local Similarity 27.6%; Pred. No. 1.4;
Matches 42; Conservative 12; Mismatches 43; Indels 55; Gaps 7;

QY 11 LLLLAGA-----PAARPTPTTCYGRMRALSOEITRDF-----NL 44
Db 3 ILSLAGHQARLDARGGMLTGPTANLAPGHVQANLILPQAVAGDFLRFQCRNPKCPL 62
QY 45 LOVESEPCVRYLRLYLDIHNYCVDLKLDRFVSPPCWKVQVDSLKDK-----ARKLYT 101
Db 63 LAVSEPGDPS---LPELGDI-----DIRTDVPRYVRWDGKLVDPLDVRGLW- 108
QY 102 IMNSFCRDVFLDDCN-----ALEYPIV 127
Db 109 -----RDDLVAFILGCSFEAMLENGLPV 134

RESULT 8
Q9QNC4
ID Q9QNC4 PRELIMINARY; PRT; 1166 AA.
AC Q9QNC4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RNA replicase.
OS Cucumber green mottle mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Yodo;
RX MEDLINE=20403259; PubMed=10948983;
RA Tan S.-H., Nishiguchi M., Murata M., Motoyoshi F.;
RA "The genome structure of kyuri green mottle mosaic tobamovirus and its
RA comparison with that of cucumber green mottle mosaic tobamovirus.";
RL Arch. Virol. 145:1067-1079(2000).
DR GO; GO:0008174; F:RNA methyltransferase activity; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR000606; Viral_helicase1.
DR InterPro; IPR002588; V_methyltransf.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
DR Pfam; PF01660; Vmethyltransf; 1.
SQ SEQUENCE 1670 AA; 188728 MW; 679269AB0ED5DE40 CRC64;

Query Match 10.7%; Score 77.5; DB 12; Length 1670;
Best Local Similarity 28.8%; Pred. No. 22;
Matches 21; Conservative 12; Mismatches 17; Indels 23; Gaps 4;

QY 59 PRLYLDIHNYCVDLKLDRFVSPPCW-----KVAQVDSLKDKARKLYTIMNSFCRR--- 109
Db 521 PELFMDFH-----DFLSA--AWEADAKIEAANVESVLDASDRLYTTVNELCERYSG 569
QY 110 ---DLVFLDDCN 119
Db 570 IEPDLEKFTDFCH 582

RESULT 10
Q9VZY2
ID Q9VZY2 PRELIMINARY; PRT; 1473 AA.
AC Q9VZY2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG32296 protein.
GN CG32296 OR CG12188 OR CG14951.
OS Drosophila melanogaster (Fruit fly).

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Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[4]
RN SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS003475; AAF47681.2; --
DR FlyBase; FBgn0052296; CG32296.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR004018; RPEL repeat.
DR InterPro; IPR003034; SAP.
DR Pfam; PF02755; RPEL; 2.
DR Pfam; PF02037; SAP; 1.
DR SMART; SM00513; SAP; 1.
DR PROSITE; P55080; SAP; 1.
SQ SEQUENCE 1473 AA; 158697 MW; 1005080E0BA7DA5F2 CRC64;

Query Match 10.4%; Score 75.5; DB 5; Length 1473;
Best Local Similarity 20.9%; Pred No. 32;
Matches 41; Conservative 21; Mismatches 65; Indels 69; Gaps 7;

QY 4 PGFLPVLL-----LLLAGAPAAAPTPTTCYSRMRLSQRITDFN 43
Db 449 PAPAPISLPTNTISITSSGGAPLNFGDATMLTPTPAATPTPT-LSLIAAPQOQLHQH 507
QY 44 LLQVSEPS-----EPCVYLPFLYLDHNYCVLDKL----- 74
Db 508 HQQLHQPTVQHPHPLSPALSSVSSIPSPATSYAESTTSSITDLARLEKMKVSDLKQH 567
QY 75 ---RDFVASPCWKVAQVDSLK-----DKARKLYTWNVSCRDLDVFLLD-----D 117
Db 568 LKRRLLPVGSP--KPHLERLKPYLPLEPLDSNVTPTAPTSNNSTTPEVITISDAMTSN 625
QY 118 CNALEYPIPVTVLPD 133
Db 626 CGLLEQPPPTMLVSD 641

RESULT 11
Q96EF3 PRELIMINARY; PRT; 300 AA.
ID AC Q96EF3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Coagulation factor XII) (Hageman factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA Kauline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC012390; AAH12390.1; --
DR EMBL; BT007350; AAP36014.1; --
DR HSSP; P00761; IAN1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.

Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]
RN SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bernan B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[4]
RN SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon K.C., Rogers J.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fouts C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.F., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svireks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RN Science 287:2185-2195 (2000).
[2]
RN SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon K.C., Rogers Y.,
RA Ranzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam G., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svireks R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[5]
RN SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bernan B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

```

DR GO:0004295; F:trypsin activity; IEA.
DR GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR009003; Cys Ser trypsin.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS0134; TRYPSIN_HIS; 1.
DR PROSITE: PS0135; TRYPSIN_SER; 1.
KW Hypothetical protein; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 300 AA; 32216 MW; PFC2BDF9382F636A CRC64;

Query Match 10.3%; Score 75; DB 4; Length 300;
Best Local Similarity 25.5%; Pred. No. 6.3;
Matches 26; Conservative 12; Mismatches 36; Indels 28; Gaps 5;

QY 2 RTGGLPVLVLLLAGAPAAAPTTP-----TCYSRMALSQEITRDFNLLQVSEPSSEP 53
Db 21 QTPGAL-----PAKEQPPSLTRNGPLSCGQRLKSLSSMTRVVGGLVALRGAHP 70

QY 54 CVRYLPRLYLDIHNYCVLDKLRDFVASPPCKVQAQVDSLKDK 95
Db 71 ---YIAALYWG-HSFCAGSLI-----APCWVLTAAHCLQDR 102

RESULT 12
Q9TDS6 PRELIMINARY; PRT; 348 AA.
AC Q9TDS6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit II.
OS Leptolebias minimus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Leptolebias.
OX NCBI_TaxID=50314;
RN [1]
RP SEQUENCE FROM N.A.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective."
RL Evolution 53:1200-1216(1999).
DR EMBL: AF092364; AAF02926.1; -.
DR GO:0005739; C:mitochondrion; IEA.
DR GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO:0016491; F:oxidoreductase activity; IEA.
DR GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro: IPR03917; NADHub_oxid2.
DR InterPro: IPR001750; Oxidored gl.
DR Pfam: PF00361; oxidored gl. 1.
DR PRINTS: PR01436; NADHDHGNASE2.
KW NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
SQ SEQUENCE 348 AA; 38796 MW; 5CB874C94B87723E CRC64;

Query Match 10.3%; Score 75; DB 8; Length 348;
Best Local Similarity 24.4%; Pred. No. 7.4;
Matches 33; Conservative 18; Mismatches 48; Indels 36; Gaps 5;

QY 6 PLVPLVLLLAGAPAAAPTTPCTYSRMALSQEITRDFNLLQVSEPSPCVRYLPRLYL-- 63
Db 194 PFSFILAFVAVMYVVGUTMPVFF-----ALNYMQTKNINILSISRSKAPFLFSLMLPYLLS 249

QY 64 -----DIHNYCVLDKLRDFVASPPCKVQAQVDSLKDKARKLYTIMNSFCERDLVFL 114
Db 250 LGGLPPSGFLPKWMLDKLTDYAKPVAVAA-----LFTLLSLF-----FY 292

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QY 115 LDDCNALFPIPIVPTT 129
Db 293 L-----RLSYTTALT 303

RESULT 13
Q81ZS5 PRELIMINARY; PRT; 615 AA.
AC Q81ZS5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coagulation factor XII-Mie.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada H., Nishio K., Nakatani K., Kasai Y., Abe Y., Nobori T.;
RT "Molecular characterization of coagulation factor XII-Mie."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB093845; BAC23095.1; -.
DR GO:0005576; C:extracellular; IEA.
DR GO:0005509; F:calcium ion binding; IEA.
DR GO:0004263; F:chymotrypsin activity; IEA.
DR GO:0004295; F:trypsin activity; IEA.
DR GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR009003; Cys Ser trypsin.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR000083; Fibnctnl.
DR InterPro: IPR000562; FN_Type_II.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00039; fnl; 1.
DR Pfam: PF00040; fn2; 1.
DR Pfam: PF00051; kringle; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00013; ENTPEII.
DR PRINTS: PR00018; KRINGLE.
DR ProDom: PD000995; FN_Type_II; 1.
DR ProDom: PD000395; Kringle; 1.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00179; EGF_CA; 2.
DR SMART: SM00058; FNI; 1.
DR SMART: SM00059; FN2; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00022; EGF_1; 2.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01253; FIBONECTIN_1; 1.
DR PROSITE: PS00023; FIBONECTIN_2; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 615 AA; 67735 MW; 030508870A0C7EDB CRC64;

Query Match 10.3%; Score 75; DB 4; Length 615;
Best Local Similarity 25.5%; Pred. No. 14;
Matches 26; Conservative 12; Mismatches 36; Indels 28; Gaps 5;

QY 2 RTGGLPVLVLLLAGAPAAAPTTP-----TCYSRMALSQEITRDFNLLQVSEPSSEP 53
Db 336 QTPGAL-----PAKEQPPSLTRNGPLSCGQRLKSLSSMTRVVGGLVALRGAHP 385

QY 54 CVRYLPRLYLDIHNYCVLDKLRDFVASPPCKVQAQVDSLKDK 95

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Db      386  ---YIAALWYG-HSFCAGSLI-----APCWVLTAAHCLQDR 417
                                         ||| : |::|
                                         :   :   :
RESULT 14
Q91E48 PRELIMINARY; PRT; 1166 AA.
ID Q91E48 AC
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DE 131 kDa replicase.
GN REPLICASE.
OS Kyuri green mottle mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=111970;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=KGMV-C1;
RA Yoon J.Y., Min B.E., Choi S.H., Ryu K.H.;
RT Completion of nucleotide sequence and generation of highly infectious
RT transcripts to cucurbits from full-length cDNA clone of Kyuri green
RT mottle mosaic virus."
RL Arch. Virol. 146:0-0(2001).
DR EMBL; AJ295948; CAC4967.1; -.
DR GO; GO:0008174; F:mRNA methyltransferase activity; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR000606; Viral helicase1.
DR InterPro; IPR002588; V_methyltransf.
DR Pfam; PF01443; Viral helicase1; 1.
DR Pfam; PF01660; Vmethyltransf; 1.
SQ SEQUENCE 1166 AA; 131485 MW; B55A87EFA9414834 CRC64;

```

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Query Match      10.3%; Score 75; DB 12; Length 1166;
Best Local Similarity 24.2%; Pred. No. 28;
Matches 30; Conservative 20; Mismatches 36; Indels 38; Gaps 5;

QY      29  SRMRALSOEI-TRDFNLQ-----VSEPSPC-----VRYLPRL 61
Db      466  AQTEIASEKIVTQFQGLELAKVKSEAFEGCNATIIAALMSTGWFCQADELVVEAPEL 525

QY      62  YLDIHNYCVLDKLRDFVASPPCKVAQVDSLKKARKLYITMNSFCRR-----DLVFL 115
Db      526  FMDFHDF-----LSAAFEADAKTEANVESVLDSADRLYTTVNELCRYSGIEFDLEKFT 580

QY      116  DDCN 119
Db      581  DFCH 584

RESULT 15
Q91E49
IID Q91E49 PRELIMINARY; PRT; 1670 AA.
Q91E49;
DIT 01-DEC-2001 (TrEMBLrel. 19, Created)
DIT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DIT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DIT 189 kDa replicase.
GN REPLICASE.
OS Kyuri green mottle mosaic virus.
OC Viruses; SARNA positive-strand viruses, no DNA stage; Tobamovirus.
OC NCBI_TaxID=111970;
RN [1]_TaxID=111970;
SEQUENCE FROM N.A.
RRC STRAIN=KGMV-C1;
RRP Yoon J.Y., Min B.E., Choi S.H., Ryu K.H.;
ERR "Completion of nucleotide sequence and generation of highly infectious
FRT transcripts to cucurbits from full-length cDNA clone of Kyuri green
FRT mottle mosaic virus.";
FRL Arch. Virol. 146:0-0(2001).

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:08:07 ; Search time 20 Seconds
(without alignments)
658.912 Million cell updates/sec

Title: US-10-023-282-310
Perfect score: 137
Sequence: 1 MPTGPGPLVLLLLLAGAPAA.....CNALEYPIPTVTTLPRQX 137

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78:*
1: Piri:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	5.8	114	2 S45541	hypothetical prote
2	8	5.8	351	2 S20078	NOV protein - chic
3	8	5.8	361	1 HLRB	MHC class I histoc
4	8	5.8	361	2 I46858	MHC class I RLA pr
5	8	5.8	405	2 A60534	P2B/LAMP-1 precurs
6	8	5.8	451	2 S78104	lipoprotein - Stre
7	8	5.8	582	2 I38028	matrix metalloprot
8	8	5.8	582	2 I48673	matrix metalloprot
9	8	5.8	582	2 I84471	matrix metalloprot
10	8	5.8	604	2 F69802	ABC transporter (A
11	8	5.8	650	1 JCL1450	fibroblast growth
12	8	5.8	759	2 G86506	hypothetical prote
13	8	5.8	759	2 G72115	hypothetical prote
14	8	5.8	4563	1 LPHUB	apolipoprotein B-1
15	7	5.1	50	2 G89984	hypothetical prote
16	7	5.1	52	2 S05488	alpha-amylase (EC
17	7	5.1	58	2 S05489	alpha-amylase (EC
18	7	5.1	92	2 PV0007	hypothetical prote
19	7	5.1	100	2 JH0200	macrophage inflamm
20	7	5.1	100	2 S21467	macrophage inflamm
21	7	5.1	100	2 I55614	macrophage inflamm
22	7	5.1	109	2 C83453	conserved hypothet
23	7	5.1	143	1 A60159	interleukin-3 prec
24	7	5.1	149	2 B82017	probable integral
25	7	5.1	149	2 B81002	conserved hypothet
26	7	5.1	150	2 C86224	hypothetical prote
27	7	5.1	152	1 A24427	interleukin-3 prec
28	7	5.1	152	1 S42720	interleukin-3 prec
29	7	5.1	152	1 B24427	interleukin-3 prec

30	7	5.1	170	2 B97004	ferritin-like prot
31	7	5.1	172	2 T02055	pathogenesis relat
32	7	5.1	204	2 T05636	hypothetical prote
33	7	5.1	219	2 A10886	Deda-family integr
34	7	5.1	220	2 AB0084	probable Deda-fam
35	7	5.1	220	2 S48450	hypothetical prote
36	7	5.1	222	2 C75342	conserved hypothet
37	7	5.1	230	2 AC0888	probable membrane
38	7	5.1	231	2 F83186	hypothetical prote
39	7	5.1	236	2 A75530	cytochrome c-type
40	7	5.1	258	2 B72697	hypothetical prote
41	7	5.1	260	1 A36299	transcription fact
42	7	5.1	260	2 D75404	phosphatidylglycer
43	7	5.1	263	2 S57346	interleukin 15 rec
44	7	5.1	264	2 T35056	probable integral
45	7	5.1	267	2 S27953	Mx protein - pig

ALIGNMENTS

RESULT 1
S45541
hypothetical protein ypuD - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-Jul-2000
C;Accession: S45541; C69942
R;Sorokin, A.; Zumstein, E.; Azevedo, V.; Ehrlich, S.D.; Serror, P.
submitted to the EMBL Data Library, November 1993
A;Reference number: S45533
A;Accession: S45541
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <SOR>
A;Cross-references: EMBL:L09228; NID:G410114; PIDN:AAA67479.1; PID:G410123
R;Kunst, R.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Ogaulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, J
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M
Koetter, P.; Koningsreiter, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scall
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyar
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C69942
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-114 <KUN>
A;Cross-references: GB:Z99116; GB:AL009126; NID:G2634723; PIDN:CAB14262.1; PID:el1855
A;Experimental source: strain 168
C;Genetics:
A;Gene: ypuD
C;Superfamily: Bacillus subtilis hypothetical protein ypuD

Query Match 5.8%; Score 8; DB 2; Length 114;
Best Local Similarity 100.0%; Pred No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VLLLLLAG 16
| | | | |
Db 13 VLLLLLAG 20

RESULT 2
S20078
NOV protein - chicken

C:Species: Gallus gallus (chicken)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 A:Accession: S20078
 R:Joliot, V.; Martinier, C.; Dambrine, G.; Plassiart, G.; Brieac, M.; Crochet, J.; Perh
 Mol. Cell. Biol. 12, 10-21, 1992
 A:Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in myel
 A:Reference number: S20078; MUID:92107157; PMID:1309586
 A:Accession: S20078
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-351 <JOL>
 A:Cross-references: EMBL:X59284; NID:g63702; PIDN:CAA41975.1; PID:g63703
 C:Genetics:
 A:Gene: NOV

Query Match 5.8%; Score 8; DB 2; Length 351;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLL 14
 |||||
 Db 9 LPVLLLL 16

RESULT 3

HURB

MHC class I histocompatibility antigen RLA alpha chain precursor (RL-5) - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 22-Jun-1999
 A:Accession: A02193
 R:Tykocinski, M.L.; Marche, P.N.; Max, E.E.; Kindt, T.J.
 J. Immunol. 133, 2261-2269, 1984
 A:Title: Rabbit class I MHC genes: cDNA clones define full-length transcripts of an expr
 A:Reference number: A02193; MUID:84290724; PMID:6432910
 A:Accession: A02193

A:Molecule type: mRNA
 A:Residues: 1-361 <TYK>
 A:Cross-references: GB:K02441; NID:gl293894; PIDN:AAA98729.1; PID:g165496
 A:Note: The source of this protein is a T-lymphoid cell line (RL-5), which has been tran
 C:Comment: In contrast to the many antigens expressed in mouse (K, D, and L) and human
 MHC may therefore differ from the HLA and H-2 loci in having limited complexity.
 C:Superfamily: class I histocompatibility antigen; heterodimer; transmembrane protein
 C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-361/Product: class I histocompatibility antigen RLA alpha chain #status predicted <
 F:25-307/Domain: extracellular #status predicted <EXT>
 F:25-114/Domain: alpha-1 <EX1>
 F:115-206/Domain: alpha-2 <EX2>
 F:220-285/Domain: immunoglobulin homology <IMM>
 F:308-329/Domain: transmembrane #status predicted <TM>
 F:330-361/Domain: intracellular #status predicted <INT>
 F:110/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:125-188,227-283/Disulfide bonds: #status predicted

Query Match 5.8%; Score 8; DB 1; Length 361;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLL 17
 |||||
 Db 9 LLLLLL 16

RESULT 4

I46858

MHC class I RLA precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 21-Jan-2000
 A:Accession: I46858
 R:Marche, P.N.; Tykocinski, M.L.; Max, E.E.; Kindt, T.J.
 Immunogenetics 21, 71-82, 1985
 A:Title: Structure of a functional rabbit class I MHC gene: Similarity to human class I
 A:Reference number: I46858; MUID:85103547; PMID:3917974

A:Accession: I46858
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-361 <MAR>
 A:Cross-references: GB:K02819; NID:g165497; PIDN:AAA98730.1; PID:g165498
 C:Genetics:
 A:Introns: 25/1; 115/1; 207/1; 299/1; 337/1; 348/1
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 5.8%; Score 8; DB 2; Length 361;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLL 17
 |||||
 Db 9 LLLLLL 16

RESULT 5

A60534

P2B/LAMP-1 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 03-May-1996
 A:Accession: A60534
 R:Heffernan, M.; Yousefi, S.; Dennis, J.W.
 Cancer Res. 49, 6077-6084, 1989
 A:Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastat
 A:Reference number: A60534; MUID:90002989; PMID:2676155
 A:Accession: A60534
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-405 <HEF>
 C:Superfamily: lysosome-associated membrane protein

Query Match 5.8%; Score 8; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VLLLLL 16
 |||||
 Db 9 VLLLLL 16

RESULT 6

S78104

lipoprotein - Streptomyces antibioticus
 C:Species: Streptomyces antibioticus
 C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 22-Oct-1999
 A:Accession: S78104; S33183
 R:Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.
 submitted to the EMBL Data Library, September 1993
 A:Description: Characterization of a Streptomyces antibioticus gene cluster encoding a
 A:Reference number: S78104
 A:Accession: S78104
 A:Molecule type: DNA
 A:Residues: 1-451 <HER>
 A:Cross-references: EMBL:Z22577; NID:g404284; PIDN:CAA80300.1; PID:g404285
 A:Experimental source: strain ATCC 11891
 A:Note: this is a revision to the sequence from reference S33182
 R:Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.
 submitted to the EMBL Data Library, April 1993
 A:Description: Characterization of a Streptomyces antibioticus gene cluster encoding a
 A:Reference number: S33182
 A:Accession: S33183
 A:Molecule type: DNA
 A:Residues: 1-422, 'LPALTR', 429-430, 'AY', 433, 'AQE', 437, 'EIVE', 444, 'Q', 446-447, 'VYRRRRDH
 A:Cross-references: EMBL:Z22577
 A:Experimental source: strain ATCC 11891
 A:Note: this sequence has been revised in reference S78104

Query Match 5.8%; Score 8; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VLLLLLAG 16
 11 VLLLLLAG 18

Db

RESULT 7
 I38028
 matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
 N:Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase
 C:Species: Homo sapiens (man)
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000
 C:Accession: I38028; G02274; I38046; S78011; S45341; S71384
 R:Will, H.; Hinzmann, B.
 Eur. J. Biochem. 231, 602-608, 1995
 A:Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloproteinase
 A:Reference number: I38028; MUID:95377289; PMID:7649159
 A:Accession: I38028
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-582 <WILL>
 A:Cross-references: EMBL:Z48481; NID:9963053; PIDN:CAA88372.1; PID:9963054
 R:Lu, G.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00963
 A:Accession: G02274
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-582 <LUO>
 A:Cross-references: EMBL:U41078; NID:g1127836; PIDN:AAA83770.1; PID:g1127837
 R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
 Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
 A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells
 A:Reference number: I38046; MUID:95224014; PMID:7708715
 A:Accession: I38046
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7, 'S', '9-582 <OKA>
 A:Cross-references: EMBL:X83535; NID:g804993; PIDN:CAA58519.1; PID:g804994
 R:Seiki, M.
 submitted to the EMBL Data Library, January 1994
 A:Reference number: S78011
 A:Accession: S78011
 A:Molecule type: mRNA
 A:Residues: 1-7, 'S', '9-337, 'K', '339-582 <SEI>
 A:Cross-references: EMBL:D26512; NID:g793762; PIDN:BAA05519.1; PID:g793763
 R:Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shinagawa, A.; Yamamoto, E.; Seiki, M.
 Nature 370, 61-65, 1994
 A:Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
 A:Reference number: S45341; MUID:94286011; PMID:8015608
 A:Accession: S45341
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-7, 'S', '9-188, 'R', '190, 'A', '192-267, 'K', '269-272, 'HY', '275, 'P', '277-285, 'KQ', '288,
 A:Cross-references: EMBL:D26512
 R:Sato, H.; Kinoshita, T.; Takino, T.; Nakayama, K.; Seiki, M.
 FEBS Lett. 393, 101-104, 1996
 A:Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
 A:Reference number: S71384; MUID:96397540; PMID:8604434
 A:Accession: S71384
 A:Molecule type: protein
 A:Residues: 112-116 <SAW>
 C:Genetics:
 A:Gene: GDB:MMP14; MT1-MMP
 A:Cross-references: GDB:375731; OMIM:600754
 A:Map position: 14q11-14q12
 C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-97/Domain: activation peptide #status predicted <PRO>
 F:61-284/Domain: matrix metalloproteinase homology <MMP>
 F:98-582/Product: matrix metalloproteinase 14 membrane type #status predicted <MAT>

F:285-313/Domain: hinge #status predicted <HNG>
 F:314-508/Domain: hemopexin repeat homology <PXN>
 F:539-562/Domain: transmembrane #status predicted <TMX>
 F:93,239,243,249/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
 F:130/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
 F:240/Active site: Glu #status predicted
 F:319-508/Disulfide bonds: #status predicted

Query Match 5.8%; Score 8; DB 2; Length 582;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
 544 LPVLLLLL 551

RESULT 8

I48673
 matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
 C:Accession: I48673
 R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
 Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
 A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal
 A:Reference number: I38046; MUID:95224014; PMID:7708715
 A:Accession: I48673
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-582 <RES>
 A:Cross-references: EMBL:X83536; NID:g804999; PIDN:CAA58520.1; PID:g805000
 C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
 C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-97/Domain: activation peptide #status predicted <PRO>
 F:61-284/Domain: matrix metalloproteinase homology <MMP>
 F:313-508/Domain: hemopexin repeat homology <PXN>
 F:93,239,243,249/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
 F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
 F:240/Active site: Glu #status predicted

Query Match 5.8%; Score 8; DB 2; Length 582;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
 544 LPVLLLLL 551

RESULT 9

I84471
 matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
 N:Alternate names: membrane-type matrix metalloproteinase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
 C:Accession: I84471; I61946
 R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
 Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
 A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal
 A:Reference number: I38046; MUID:95224014; PMID:7708715
 A:Accession: I84471
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-582 <RES>
 A:Cross-references: EMBL:X83537; NID:g805012; PIDN:CAA58521.1; PID:g805013
 A:Accession: I61946
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-67, 'M', '69-254, 'A', '256-582 <RE2>
 A:Cross-references: EMBL:X91785; NID:g1001926; PIDN:CAA62897.1; PID:g1001927

C:Genetics:

A:Gene: mt-mmp
 A:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; zinc; zymogen
 C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-97/Domain: activation peptide #status predicted <PRO>
 F:61-284/Domain: matrix metalloproteinase homology <MMP>
 F:313-508/Domain: hemopexin repeat homology <PN>
 F:93-239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
 F:240/Active site: Glu #status predicted

Query Match 5.8%; Score 8; DB 2; Length 582;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLL 14
 |||||
 DB 544 LPVLLLLL 551

RESULT 10

F69802
 ABC transporter (ATP-binding protein) homolog yfiC - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
 C:Accession: F69802
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Enrich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabel, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
 A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Xoeiter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Ser
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; PMID:98044033; PMID:9384377
 A:Accession: F69802
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-604 <KUN>
 A:Cross-references: GB:Z99108; GB:AL009126; NID:G2633055; PIDN:CAB12651.1; PID:G2633146
 A:Experimental source: strain 168
 C:Genetics:

A:Gene: yfiC
 C:Superfamily: Escherichia coli ABC transporter mdla; ATP-binding cassette homology
 C:Keywords: ATP; nucleotide binding; P-loop
 F:382-576/Domain: ATP-binding cassette homology <ABC>
 F:399-406/Region: nucleotide-binding motif A (P-loop)

Query Match 5.8%; Score 8; DB 2; Length 604;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVLLLLLA 15
 |||||
 DB 88 PVLLLLLA 95

RESULT 11

JC1450
 fibroblast growth factor receptor 4 - rat
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-2000
 C:Accession: JC1450; PT0191
 R:Horlick, R.A.; Stack, S.L.; Cooke, G.M.

Gene 120, 291-295, 1992

A:Title: Cloning, expression and tissue distribution of the gene encoding rat fibroblas
 A:Reference number: JC1450; MUID:93013049; PMID:1398143
 A:Accession: JC1450
 A:Molecule type: mRNA
 A:Residues: 1-650 <HOR>
 A:Cross-references: GB:M91599; NID:G204137; PIDN:AAA41157.1; PID:G204138
 R:Lai, C.; Lemke, G.
 Neuron 6, 691-704, 1991
 A:Title: An extended family of protein-tyrosine kinase genes differentially expressed :
 A:Reference number: PT0183; MUID:91222560; PMID:2025425

A:Accession: PT0191
 A:Molecule type: mRNA
 A:Residues: 465-518 <LAI>
 A:Experimental source: sciatic nerve
 C:Genetics:

A:Gene: FGFR4; tyro-9

C:Function:

A:Description: receptor mediating effects of fibroblast growth factor

A:Note: expressed in normal lung; expressed in some carcinomas

C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; pro

C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor recepto

F:11-72/Domain: immunoglobulin homology <IM1>

F:110-181/Domain: immunoglobulin homology <IM2>

F:218-238/Domain: transmembrane #status predicted <TMM>

F:239-650/Domain: intracellular #status predicted <INT>

F:313-598/Domain: protein kinase homology <KIN>

F:321-329/Region: protein kinase ATP-binding motif

F:104,136,157,168/Binding site: carboxylate (Asn) (covalent) #status predicted

F:351,368,460/Active site: Lys, Glu, Asp #status predicted

F:465,478/Binding site: magnesium (Asn, Asp) #status predicted

F:493/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict

Query Match 5.8%; Score 8; DB 1; Length 650;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VLLLLLAG 16
 |||||
 DB 229 VLLLLLAG 236

RESULT 12

GB6506
 hypothetical protein CPJ0126 [imported] - Chlamydomophila pneumoniae (strain J138)
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: GB6506

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T. ;
 Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: GB6506

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-759 <STO>

A:Cross-references: GB:BA000008; NID:G9878500; PIDN:BAA98337.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: CPJ0126

Query Match 5.8%; Score 8; DB 2; Length 759;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VLLLLLAG 16
 |||||
 DB 37 VLLLLLAG 44

RESULT 13

G72115
 hypothetical protein CP0646 [imported] - Chlamydomophila pneumoniae (strains CWL029 and ;

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 A:Accession: G72115; F01554
 R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammell, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
 A>Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: G72115
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-759 <ARN>
 A:Cross-references: GB:AE001599; GB:AE001363; NID:G4376387; PIDN:AAD18279.1; PID:G437638
 A:Experimental source: strain CWL029
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: F81554
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-759 <REA>
 A:Cross-references: GB:AE002222; GB:AE002161; NID:G7189553; PIDN:AAF38461.1; PID:G718955
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CPN0126; CP0646

Query Match 5.8%; Score 8; DB 2; Length 759;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VILLIAG 16
 |||||
 Db 37 VILLIAG 44

RESULT 14
 LPHUB
 apolipoprotein B-100 precursor - human
 N:Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
 C:Species: Homo sapiens (man)
 C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 21-Jul-2000
 A:Accession: A27850; A25679; A25267; A24320; A24684; A23817; A25774; A284452; I61909; I59510; I39474; I39469; I84624; I37179; P50058
 R:Luwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Soc DNA 6, 363-372, 1987
 A>Title: DNA sequence of the human apolipoprotein B gene.
 A:Reference number: A27850; MUID:88003974; PMID:3652907
 A:Accession: A27850
 A:Molecule type: DNA
 A:Residues: 1-617, 'A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431, 'Q', 3433-3731, 'A'
 A:Cross-references: GB:M14162
 R:Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I. EMBO J. 5, 3495-3507, 1986
 A>Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
 A:Reference number: A91058; MUID:87161758; PMID:3030729
 A:Accession: A25679
 A:Molecule type: mRNA
 A:Residues: 1-11, 15-2539, 'S', 2541-3823, 'R', 3825-4563 <CLA>
 A>Note: 1109-ASP was also found
 R:Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Luisis, A.J.; Blackhart, B.; McCa Nucleic Acids Res. 14, 7501-7503, 1986
 A>Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
 A:Reference number: A93639; MUID:87016385; PMID:3763409
 A:Accession: A25263
 A:Molecule type: mRNA
 A:Residues: 1-272, 'N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679, 'Q'
 A:Cross-references: GB:X04506; NID:G34330; PIDN:CAA28191.1; PID:G34331
 R:Law, S.W.; Grant, S.M.; Higuchi, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer JH Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
 A>Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
 A:Reference number: A94134; MUID:87041416; PMID:3464946
 A:Accession: A25267

A:Molecule type: mRNA
 A:Residues: 1-617, 'A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 4189-4220, 'M', 4222-4563 <LAU>
 A>Note: The codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and R; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., J. Biol. Chem. 261, 12918-12921, 1986
 A>Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
 A:Reference number: A92556; MUID:87008488; PMID:3759943
 A:Accession: A25266
 A:Molecule type: mRNA
 A:Residues: 1-97, 'I', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3429-4132, 'G', 4134-4180, 'E', 4182-4563 <CHS>
 A:Cross-references: GB:J02610; NID:G178803; PIDN:AAA35549.1; PID:G178804
 A>Note: A total of 2366 residues were confirmed by direct sequencing of tryptic peptides; R; Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hori, Y.J.; Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986
 A>Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein B. Reference number: A24320; MUID:86287319; PMID:3461454
 A:Accession: A24320
 A:Molecule type: mRNA
 A:Residues: 1-97, 'I', 99-617, 'A', 619-941, 'Y', 943-1138, 'P', 1139-1866, 'G', 1868-2036, 'N', 4189-4220, 'M', 4222-4563 <LAU>
 A:Cross-references: GB:M14081; NID:G178795; PIDN:AAA51752.1; PID:G553189
 R:Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylon Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
 A>Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of A:Reference number: A24684; MUID:86094221; PMID:3001697
 A:Accession: A24684
 A:Molecule type: mRNA
 A:Residues: 485-617, 'A', 619-1044 <LA2>
 A:Cross-references: GB:M12480; NID:G178791; PIDN:AAA51751.1; PID:G178792
 R:Protter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
 A>Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipoprotein B. Reference number: A94088; MUID:86149325; PMID:3513177
 A:Accession: A23817
 A:Molecule type: mRNA
 A:Residues: 1-291 <PRO>
 A:Cross-references: GB:M12681; NID:G178797; PIDN:AAA51753.1; PID:G178798
 R:Deeb, S.S.; Motulsky, A.G.; Aibers, J.J. Proc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985
 A>Title: A partial cDNA clone for human apolipoprotein B.
 A:Reference number: A25774; MUID:85270450; PMID:3860836
 A:Accession: A25774
 A:Molecule type: mRNA
 A:Residues: 709-791, 'SSSWKAAASHGCPHSACD', 810-906 <DEE>
 A:Cross-references: GB:K03175; NID:G178821; PIDN:AAA51759.1; PID:G178822
 R:Carlsson, P.; Darnfors, C.; Olofsson, S.O.; Bjursell, G. Gene 49, 29-51, 1986
 A>Title: Analysis of the human apolipoprotein B gene; complete structure of the B-74 x A:Reference number: A91565; MUID:87191999; PMID:2883086
 A:Accession: A26533
 A:Molecule type: mRNA
 A:Residues: 1282-2721, 2742-3290, 'L', 3292-3336, 'N', 3338-3948, 'F', 3950-3963, 'Y', 3965-418 A:Cross-references: GB:M15421; NID:G178817; PIDN:AAA51758.1; PID:G178818
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 A:Accession: A29671
 A:Molecule type: mRNA
 A:Residues: 1671-2323, 'PYW', 2327-2352, 'H', 2354-2398 <HAR>
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 A;Accession: A24738
 A;Molecule type: mRNA
 A;Residues: 'N', 3729-3731, 'I', 3733-3875, 'A', 3877-3948, 'F', 3950-3963, 'Y', 3965-3982, 'S', 3984-3986, 'G', 3988-3990, 'L', 3992-3994, 'P', 3996-3998, 'K', 3999-4001, 'Q', 4003-4005, 'R', 4007-4009, 'H', 4011-4013, 'D', 4015-4017, 'N', 4019-4021, 'C', 4023-4025, 'E', 4027-4029, 'G', 4031-4033, 'A', 4035-4037, 'S', 4039-4041, 'P', 4043-4045, 'T', 4047-4049, 'K', 4051-4053, 'R', 4055-4057, 'Q', 4059-4061, 'N', 4063-4065, 'D', 4067-4069, 'K', 4071-4073, 'R', 4075-4077, 'Q', 4079-4081, 'N', 4083-4085, 'D', 4087-4089, 'K', 4091-4093, 'R', 4095-4097, 'Q', 4099-4101, 'N', 4103-4105, 'D', 4107-4109, 'K', 4111-4113, 'R', 4115-4117, 'Q', 4119-4121, 'N', 4123-4125, 'D', 4127-4129, 'K', 4131-4133, 'R', 4135-4137, 'Q', 4139-4141, 'N', 4143-4145, 'D', 4147-4149, 'K', 4151-4153, 'R', 4155-4157, 'Q', 4159-4161, 'N', 4163-4165, 'D', 4167-4169, 'K', 4171-4173, 'R', 4175-4177, 'Q', 4179-4181, 'N', 4183-4185, 'D', 4187-4189, 'K', 4191-4193, 'R', 4195-4197, 'Q', 4199-4201, 'N', 4203-4205, 'D', 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7183-7185, 'D', 7187-7189, 'K', 7191-7193, 'R', 7195-7197, 'Q', 7199-7201, 'N', 7203-7205, 'D', 7207-7209, 'K', 7211-7213, 'R', 7215-7217, 'Q', 7219-7221, 'N', 7223-7225, 'D', 7227-7229, 'K', 7231-7233, 'R', 7235-7237, 'Q', 7239-7241, 'N', 7243-7245, 'D', 7247-7249, 'K', 7251-7253, 'R', 7255-7257, 'Q', 7259-7261, 'N', 7263-7265, 'D', 7267-7269, 'K', 7271-7273, 'R', 7275-7277, 'Q', 7279-7281, 'N', 7283-7285, 'D', 7287-7289, 'K', 7291-7293, 'R', 7295-7297, 'Q', 7299-7301, 'N', 7303-7305, 'D', 7307-7309, 'K', 7311-7313, 'R', 7315-7317, 'Q', 7319-7321, 'N', 7323-7325, 'D', 7327-7329, 'K', 7331-7333, 'R', 7335-7337, 'Q', 7339-7341, 'N', 7343-7345, 'D', 7347-7349, 'K', 7351-7353, 'R', 7355-7357, 'Q', 7359-7361, 'N', 7363-7365, 'D', 7367-7369, 'K', 7371-7373, 'R', 7375-7377, 'Q', 7379-7381, 'N', 7383-7385, 'D', 7387-7389,

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OM protein - protein search, using sw model

Run on: February 25, 2004, 05:08:28 / Search time 39 Seconds
(without alignments)
1108.359 Million cell updates/sec

Title: US-10-023-282-310
Perfect score: 137
Sequence: 1 MPTGPLPVLILLAGAPAA.....CNALEYPIPTVTLVDRQX 137

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	6.6	504	13 Q9YH45	Q9YH45 gallus gall
2	9	6.6	504	13 Q90ZK6	Q90ZK6 gallus gall
3	8	5.8	71	10 Q7XUJ0	Q7XUJ0 oryza sativ
4	8	5.8	136	16 Q82R50	Q82R50 streptomyce
5	8	5.8	160	11 Q8C254	Q8C254 mus musculu
6	8	5.8	160	11 Q8C239	Q8C239 mus musculu
7	8	5.8	173	16 Q9RJ35	Q9RJ35 streptomyce
8	8	5.8	202	11 Q9QW8	Q9QW8 rattus sp.
9	8	5.8	229	11 Q8BNV8	Q8BNV8 mus musculu
10	8	5.8	232	10 Q8RUN7	Q8RUN7 oryza sativ
11	8	5.8	245	16 Q8XYW8	Q8XYW8 ralestonia s
12	8	5.8	252	4 Q9BQ73	Q9BQ73 homo sapien
13	8	5.8	258	2 Q9LA77	Q9LA77 bacillus th
14	8	5.8	281	16 Q7W5U7	Q7W5U7 bordetella
15	8	5.8	281	16 Q7W5U7	Q7W5U7 bordetella
16	8	5.8	281	16 Q7VYZ5	Q7VYZ5 bordetella

17	8	5.8	286	16 Q7WCW1	Q7WCW1 bordetella
18	8	5.8	286	16 Q7VZN4	Q7VZN4 bordetella
19	8	5.8	304	4 Q96182	Q96182 homo sapien
20	8	5.8	319	4 Q00477	Q00477 homo sapien
21	8	5.8	333	16 Q9KZW9	Q9KZW9 streptomyce
22	8	5.8	334	4 Q9NR44	Q9NR44 homo sapien
23	8	5.8	334	4 Q9BU81	Q9BU81 homo sapien
24	8	5.8	350	4 Q99420	Q99420 homo sapien
25	8	5.8	357	4 Q15338	Q15338 homo sapien
26	8	5.8	358	7 Q30849	Q30849 oryctolagus
27	8	5.8	359	4 P78410	P78410 homo sapien
28	8	5.8	368	13 Q57408	Q57408 meleagris g
29	8	5.8	380	10 Q8S0V9	Q8S0V9 oryza sativ
30	8	5.8	495	4 Q9HCY1	Q9HCY1 homo sapien
31	8	5.8	513	4 Q00481	Q00481 homo sapien
32	8	5.8	524	11 Q9D8N4	Q9D8N4 mus musculu
33	8	5.8	524	11 Q99N16	Q99N16 mus musculu
34	8	5.8	568	2 Q52723	Q52723 treponema p
35	8	5.8	582	6 Q9XSP0	Q9XSP0 capra hircu
36	8	5.8	582	6 Q9GLE4	Q9GLE4 bos taurus
37	8	5.8	582	11 Q8BTX2	Q8BTX2 mus musculu
38	8	5.8	584	16 Q8FE94	Q8FE94 xanthomonas
39	8	5.8	606	6 Q97554	Q97554 oryctolagus
40	8	5.8	650	11 Q63709	Q63709 rattus ratt
41	8	5.8	693	10 Q8S7C8	Q8S7C8 oryza sativ
42	8	5.8	693	10 Q7XC16	Q7XC16 oryza sativ
43	8	5.8	759	16 Q9Z955	Q9Z955 chlamydia p
44	8	5.8	759	16 Q7VQ78	Q7VQ78 chlamydia p
45	8	5.8	782	10 Q9LDJ6	Q9LDJ6 oryza sativ

ALIGNMENTS

RESULT 1

Q9YH45 PRELIMINARY; PRT; 504 AA.
AC Q9YH45;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Type I TGF B receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Leghorn; TISSUE=Heart;
RA Brame G.P., Barnett J.V.;
RT "Cloning and Expression of a Type I TGF B Receptor.";
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U38622; AAC98806.1; -;
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005024; F:transforming growth factor-beta receptor ac. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.
DR InterPro; IPR000472; Activin receptor.
DR InterPro; IPR000333; Actn_receptoril.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR003605; TGFbeta_GS.
DR Pfam; PF01064; Activin_recip; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 504 AA; 56240 MW; 6ACEED700DDC7A32 CRC64;

Query Match 6.6%; Score 9; DB 13; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLLA 15
Db 3 LPVLLLLLA 11

RESULT 2
Q90ZK6 PRELIMINARY; PRT; 504 AA.
AC Q90ZK6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta receptor I.
GN TGFBR1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Derco-brown;
RA Skumatava A., Schuster M.K., Edelman H.M.L., Kuchler K.;
RT "Transforming Growth Factor beta Signalling in the Avian Ovary."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ318064; CAC39433.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transforming growth factor-beta receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor-beta receptor ac. .; IEA.
DR GO; GO:0006458; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007198; P:transmembrane receptor protein serine/threo. .; IEA.
DR InterPro; IPR000472; Activin_receptor.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR003605; TGFbeta_GS.
DR Pfam; PF01064; Activin_recpt.1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00053; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 504 AA; 56224 MW; C7F045D6A25A071E CRC64;

Query Match 6.6%; Score 9; DB 13; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLLA 15
Db 3 LPVLLLLLA 11

RESULT 3
Q7XUJ0 PRELIMINARY; PRT; 71 AA.
ID Q7XUJ0
AC Q7XUJ0

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNB0103108.13 protein.
GN OSJNB0103108.13.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Ma J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.H., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606695; CAD41274.1; -
SQ SEQUENCE 71 AA; 7480 MW; 64AC2D1ACAF7F805 CRC64;

Query Match 5.8%; Score 8; DB 10; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVLLLLLA 14
Db 25 LPVLLLLLA 32

RESULT 4
Q82R50 PRELIMINARY; PRT; 136 AA.
ID Q82R50
AC Q82R50
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative invasion protein.
GN SAV294.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites".
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis".
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005022; BAC68003.1; -
KW Complete proteome.
SQ SEQUENCE 136 AA; 13687 MW; 8273376F70E3EBE7 CRC64;

Query Match 5.8%; Score 8; DB 16; Length 136;
Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLLAGA 17
 Db 96 LLLLLLAGA 103

RESULT 5

Q8C254 PRELIMINARY; PRT; 160 AA.
 AC Q8C254; 2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Weakly similar to TREM-1.
 GN A530064D06RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD;
 RX MEDLINE=22354683; PubMed=12466851;
 RA the FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 DR ENBL; AK089248; BAC40812.1; --
 DR MGD; MGI:2443476; A530064D06RIK.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 SQ SEQUENCE 160 AA; 19501 MW; B66C1AA8D129921B CRC64;

Query Match 5.8%; Score 8; DB 11; Length 160;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVLILLILA 15
 Db 11 PVLILLILA 18

RESULT 6

Q8C239 PRELIMINARY; PRT; 160 AA.
 AC Q8C239; 2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Weakly similar to TREM-1.
 GN A530064D06RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J;
 RX MEDLINE=22354683; PubMed=12466851;
 RA the FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 DR ENBL; AK089332; BAC40844.1; --
 DR MGD; MGI:2443476; A530064D06RIK.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.

DR PROSITE; PS00835; IG LIKE; 1.
 SQ SEQUENCE 160 AA; 18487 MW; B663FAB2D1299201 CRC64;

Query Match 5.8%; Score 8; DB 11; Length 160;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVLILLILA 15
 Db 11 PVLILLILA 18

RESULT 7

Q9RJ35 PRELIMINARY; PRT; 173 AA.
 AC Q9RJ35;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2003 (TREMBlrel. 23, Last annotation update)
 DE Putative membrane protein.
 GN SCO1833 OR SC18.18C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinomycetaceae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR ENBL; AL939110; CAB59449.1; --
 KW Complete proteome.
 SQ SEQUENCE 173 AA; 18906 MW; 8E48D377AFC302B0 CRC64;

Query Match 5.8%; Score 8; DB 16; Length 173;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLLAGA 17
 Db 12 LLLLLLAGA 19

RESULT 8

Q9QVW8 PRELIMINARY; PRT; 202 AA.
 AC Q9QVW8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Fibroblast growth factor receptor 4, FGFR-4 (fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94293355; PubMed=8021968;
 RA Yazaki N., Hosoi Y., Kawabata K., Miyake A., Minami M., Satoh M.,
 RA Ohta M., Kawasaki T., Itoh N.;
 RT "Differential expression patterns of mRNAs for members of the
 RT fibroblast growth factor receptor family, FGFR-1-FGFR-4, in rat

DE	P0435B05.27 protein (P0503C12.6 protein).	DE	P0435B05.27 OR P0503C12.6.
GN	J. Neurosci. Res. 37:445-452 (1994).	GN	Oryza sativa (japonica cultivar-group).
OS	HSP: P11362; IFGK.	OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	GO: GO:0005524; F:ATP binding; IEA.	OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	GO: GO:0004672; F:protein kinase activity; IEA.	OC	Ehrhartoidae; Oryzae; Oryza.
OC	GO: GO:0016740; F:transferase activity; IEA.	OX	NCBI_TaxID=39947;
OC	GO: GO:0006468; P:protein amino acid phosphorylation; IEA.	RN	[1]
OC	InterPro; IPR007110; IG-like.	RP	SEQUENCE FROM N.A.
OC	InterPro; IPR007119; Prot.kinase.	RC	STRAIN=cv. Nipponbare;
OC	Pfam; PF00069; pkinase; 1.	RA	Sasaki T., Matsumoto T., Yamamoto K.;
OC	PRODOM; PD000001; Prot.kinase; 1.	RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
OC	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	RT	clone:P0435B05.";
OC	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.	RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
KW	ATP-binding; Transferase.	DR	EMBL; AP003249; BAB89548.1; -.
FT	NON_TER 1	DR	EMBL; AP003268; BAB89682.1; -.
FT	NON_TER 202	DR	Gramene; Q8RUN7; -.
FT	NON_TER 202	SQ	SEQUENCE 232 AA; 24813 MW; 9EEA7B33EB03C787 CRC64;
SQ	SEQUENCE 202 AA; 21986 MW; 8F87690566EBAF31 CRC64;	Query Match	5.8%; Score 8; DB 10; Length 232;
Query Match	5.8%; Score 8; DB 11; Length 202;	Best Local Similarity	100.0%; Pred.No. 9.8;
Best Local Similarity	100.0%; Pred.No. 8.7; 0; Indels 0; Gaps 0;	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	10 LLLLLLAG 17
QY	9 VLLLLLAG 16	DB	46 LLLLLLAG 53
DB	58 VLLLLLAG 65	RESULT 11	
RESULT 9		Q8XYW8	PRELIMINARY; PRT; 245 AA.
Q8BNV8	PRELIMINARY; PRT; 229 AA.	ID	Q8XYW8
AC	Q8BNV8	AC	Q8XYW8
DT	01-MAR-2003 (TremBLrel. 23, Created)	DT	01-MAR-2002 (TremBLrel. 20, Created)
DT	01-MAR-2003 (TremBLrel. 23, Last sequence update)	DT	01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT	01-OCT-2003 (TremBLrel. 25, Last annotation update)	DT	01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE	Weakly similar to TREM-1.	DE	Putative signal peptide protein.
CN	A530064D06RIK.	GN	RSC1638 OR RS04012.
OS	Mus musculus (Mouse).	OS	Ralstonia solanacearum (Pseudomonas solanacearum).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC	Burkholderiaceae; Ralstonia.
OX	NCBI_TaxID=10090;	OX	NCBI_TaxID=305;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;	RC	STRAIN=GM11000;
RX	MEDLINE=22354583; PubMed=12466851;	RX	MEDLINE=21681879; PubMed=11823852;
RA	The FANTOM Consortium,	RA	Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S.,
RA	"Analysis of the mouse transcriptome based on functional annotation of	RA	Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RT	the RIKEN Genome Exploration Research Group Phase I & II Team;	RA	Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
RT	"Analysis of the mouse transcriptome based on functional annotation of	RA	Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RT	60,770 full-length cDNAs.";	RA	Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RL	Nature 420:563-573 (2002).	RA	Weissenbach J., Boucher C.A.;
RL	EMBL; AK080114; EAC37828.1; -.	RA	"Genome sequence of the plant pathogen Ralstonia solanacearum.";
DR	MGD; MGI:2443476; A530064D06RIK.	RL	Nature 415:497-502 (2002).
DR	InterPro; IPR003599; IG.	DR	EMBL; AL646065; CAD15340.1; -.
DR	InterPro; IPR007110; IG-like.	KW	Complete proteome.
DR	SMART; SM00409; IG; 1.	SQ	SEQUENCE 245 AA; 25084 MW; 052687842114EB42 CRC64;
DR	PROSITE; PS0835; IG LIKE; 1.	Query Match	5.8%; Score 8; DB 16; Length 245;
SQ	SEQUENCE 229 AA; 25348 MW; 1DCD313A64B113F8 CRC64;	Best Local Similarity	100.0%; Pred.No. 10;
Query Match	5.8%; Score 8; DB 11; Length 229;	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity	100.0%; Pred.No. 9.7; 0; Indels 0; Gaps 0;	QY	8 PVLLLLLA 15
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DB	11 PVLLLLLA 18
QY	8 PVLLLLLA 15	RESULT 10	
DB	11 PVLLLLLA 18	Q8RUN7	PRELIMINARY; PRT; 232 AA.
RESULT 10		ID	Q8RUN7
Q8RUN7	PRELIMINARY; PRT; 232 AA.	AC	Q8RUN7
AC	Q8RUN7	DT	01-JUN-2002 (TremBLrel. 21, Created)
DT	01-JUN-2002 (TremBLrel. 21, Last sequence update)	DT	01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT	01-OCT-2002 (TremBLrel. 22, Last annotation update)	DT	01-OCT-2002 (TremBLrel. 22, Last annotation update)

RESULT 12
 Q9BQ73 PRELIMINARY; PRT; 252 AA.
 ID Q9BQ73
 AC Q9BQ73
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE FKSG28 (FKSG40).
 GN FKSG28 OR FKSG40.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang Y.-G., Gong L.;
 RT "Cloning of FKSG28, a novel gene located on human chromosome 10.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wang Y.-G., Gong L.;
 RT "Identification of FKSG40, a novel gene located on human chromosome 10.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY014271; AAG50354.1; -.
 DR EMBL; AF333487; AAG50291.1; -.
 DR HSP; P01004; 1SGP.
 DR GO; GO:0004867; F-serine protease inhibitor activity; IEA.
 DR InterPro; IPR002350; kazal.
 DR Pfam; PF00050; kazal; 1.
 DR SMART; SM00280; kazal; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 252 AA; 26525 MW; 6A9AB2C8515509B8 CRC64;

 Query Match 5.8%; Score 8; DB 4; Length 252;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 7 LPVLLLLL 14
 DB 13 LPVLLLLL 20

 RESULT 13
 Q9LAF7 PRELIMINARY; PRT; 258 AA.
 ID Q9LAF7
 AC Q9LAF7
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 2-hydroxypenta-2,4-dienoate hydratase.
 GN PHED.
 OS Bacillus thermoglucosidasius (Geobacillus thermoglucosidasius).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1426;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duffner F.M., Kirchner U., Bauer M.P., Muller R.;
 RT "Phenol/cresol degradation by the thermophilic Bacillus thermoglucosidasius A7: cloning and sequence analysis of five genes involved in the pathway.";
 RL Gene 256:215-221(2000).
 DR EMBL; AF140605; AAF66552.1; -.
 DR GO; GO:0016829; F-lyase activity; IEA.
 DR GO; GO:0006725; Paromastic compound metabolism; IEA.
 DR InterPro; IPR002607; Hydratase decarb.
 DR Pfam; PF01689; Hydratase decarb; 1.
 DR ProDom; PD003721; Hydratase decarb; 1.
 SQ SEQUENCE 258 AA; 28307 MW; 4F51770C39A360E1 CRC64;

 Query Match 5.8%; Score 8; DB 2; Length 258;

Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 43 NLLQVSEP 50
 DB 68 NLLQVSEP 75

 RESULT 14
 Q7WGJ8 PRELIMINARY; PRT; 281 AA.
 ID Q7WGJ8
 AC Q7WGJ8
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative membrane protein.
 GN BB3591.
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RB50 / ATCC BAA-588;
 RX MEDLINE=22827954; PubMed=12910271;
 RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltham D., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; BX64047; CAE34085.1; -.
 KW Complete proteome.
 SQ SEQUENCE 281 AA; 30438 MW; C8368E22B996193C CRC64;

 Query Match 5.8%; Score 8; DB 16; Length 281;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 10 LLLLLAGA 17
 DB 191 LLLLLAGA 198

 RESULT 15
 Q7WSU7 PRELIMINARY; PRT; 281 AA.
 ID Q7WSU7
 AC Q7WSU7
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative membrane protein.
 GN BPP3191.
 OS Bordetella parapertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=12822 / ATCC BAA-587;
 RX MEDLINE=22827954; PubMed=12910271;
 RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; EX640432; CAE38476.1; --
 KW Complete proteome.
 SQ SEQUENCE 281 AA; 30438 MW; C8368E22B996193C CRC64;

Query Match 5.8%; Score 8; DB 16; Length 281;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLLLAGA 17
 |||||
 Db 191 LLLLLAGA 198

Search completed: February 25, 2004, 05:12:17
 Job time : 41 secs